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L5: Entry 9 of 14 File: PGPB Oct 3, 2002

DOCUMENT-IDENTIFIER: US 20020143159 A1
TITLE: BONE MORPHOGENETIC PROTEIN (BMP)-17 AND BMP-18 COMPOSITIONS

Summary of Invention Paragraph:
[0003] Human BMP-17 and BMP-18 appear to be human homologs of a murine protein called Lefty. The nucleotide and amino acid sequences of murine Lefty are described in Zhou et al., Nature, 361:543-547 (1993). The murine Lefty gene has been described as being expressed in the mouse node during gastrulation. A related human protein, designated endometrial bleeding associated factor [EBAF] was published in Kothapelli et al., J. Clin. Invest., 99:2342-2350 (1997).

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NiceProt View of Swiss-Prot: O00292

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**TGF4_HUMAN**
Primary accession number	**O00292**
Secondary accession numbers	O75611 Q8NBQ9
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	**Transforming growth factor beta 4 [Precursor]**
Synonyms	**TGF-beta 4** **Endometrial bleeding-associated factor** **Left-right determination factor A** **Lefty-A protein**
Gene name	**Name: EBAF** Synonyms: LEFTA, LEFTYA, TGFB4
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.
TISSUE=Placenta;
MEDLINE=97298127;PubMed=9153275 [NCBI, ExPASy, EBI, Israel, Japan]
Kothapalli R., Buyuksal I., Wu S.-Q., Chegini N., Tabibzadeh S.;
"Detection of ebaf, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding.";
J. Clin. Invest. 99:2342-2350(1997).

[2] REVISIONS.
MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]
Kothapalli R.;
Unpublished results, cited by: Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,

Casey B.; Am. J. Hum. Genet. 64:712-721(1999).

[3] SEQUENCE FROM NUCLEIC ACID, AND VARIANT L-R AXIS MALFORMATIONS ASN-342.
TISSUE=Placenta;
MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]
Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;
"Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";
Am. J. Hum. Genet. 64:712-721(1999).

[4] SEQUENCE FROM NUCLEIC ACID.
DOI=10.1038/ng1285;PubMed=14702039 [NCBI, ExPASy, EBI, Israel, Japan]
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., , Sugano S.;
"Complete sequencing and characterization of 21,243 full-length human cDNAs.";
Nat. Genet. 36:40-45(2004).

[5] SEQUENCE FROM NUCLEIC ACID.
TISSUE=Ovary;
DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., , Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Comments

- ***FUNCTION***: Required for left-right (L-R) asymmetry determination of organ systems in mammals. May play a role in endometrial bleeding.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***TISSUE SPECIFICITY***: Mesenchymal cells of the endometrial stroma.
- ***DEVELOPMENTAL STAGE***: Transiently expressed before and during menstrual bleeding.
- ***PTM***: The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- ***DISEASE***: Defects in EBAF are the cause of left-right axis malformations (L-R axis malformation) [MIM:601877]. The defect includes left pulmonary isomerism, with cardiac anomalies characterized by complete atrioventricular canal defect and hypoplastic left ventricle, and interrupted inferior vena cava.
- ***SIMILARITY***: Belongs to the TGF-beta family.

Copyright

Cross-references

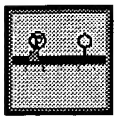
EMBL	U81523; AAB53269.1; ALT_SEQ.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081511; AAC32600.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081508; AAC32600.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081509; AAC32600.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF081510; AAC32600.1; JOINED.	[EMBL / GenBank / DDBJ] [CoDingSequence]

	AF081513; AAD48145.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AK075344; BAC11556.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	BC035718; AAH35718.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P10600; 1TGJ. [HSSP ENTRY / PDB]
Genew	HGNC:3122; EBAF.
CleanEx	HGNC:3122; EBAF.
GeneCards	EBAF.
GeneLynx	EBAF; Homo sapiens.
GenAtlas	EBAF.
H-InvDB	HIX0001640; -.
MIM	601877 [NCBI / EBI].
GO	GO:0007275; Biological process: development *(traceable author statement).* GO:0007309; Biological process: oocyte axis determination *(traceable author statement).* GO:0007179; Biological process: transforming growth factor beta receptor signaling pathway *(traceable author statement).* QuickGo view.
SOURCE	EBAF; Homo sapiens.
Ensembl	O00292; Homo sapiens. [Entry / Contig view]
InterPro	IPR001839; TGFb. IPR001111; TGFb_N. Graphical view of domain structure.
Pfam	PF00019; TGF_beta; 1. PF00688; TGFb_propeptide; 1. Pfam graphical view of domain structure.
ProDom	PD000357; TGFb; 1. [Domain structure / List of seq. sharing at least 1 domain]
PROSITE	PS00250; TGF_BETA_1; 1.
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	O00292.
ProtoNet	O00292.
ProtoMap	O00292.
PRESAGE	O00292.
DIP	O00292.
ModBase	O00292.
SMR	O00292; 63A416CAE30F7A39.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

Cytokine; **Developmental protein**; **Disease mutation**; **Glycoprotein**; **Growth factor**; **Multigene family**; **Signal**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	21	21	*Potential.*	
PROPEP	22	76	55	Or 135 (*Potential*).	
CHAIN	77	366	290	Transforming growth factor beta 4.	
DISULFID	251	264		*By similarity.*	
DISULFID	263	316		*By similarity.*	
DISULFID	293	351		*By similarity.*	
DISULFID	297	353		*By similarity.*	
CARBOHYD	158	158		N-linked (GlcNAc...) (*Potential*).	
VARIANT	342	342	*	S -> N (in L-R axis malformations).	VAR_010385
CONFLICT	183	183		A -> P (in Ref. 4).	

Sequence information

Length: **366 AA** [This is the length of the unprocessed precursor]

Molecular weight: **40920 Da** [This is the MW of the unprocessed precursor]

CRC64: **63A416CAE30F7A39** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
         |          |          |          |          |          |
MWPLWLCWAL WVLPLAGPGA ALTEEQLLGS LLRQLQLSEV PVLDRADMEK LVIPAHVRAQ

        70         80         90        100        110        120
         |          |          |          |          |          |
YVVLLRRSHG DRSRGKRFSQ SFREVAGRFL ASEASTHLLV FGMEQRLPPN SELVQAVLRL

       130        140        150        160        170        180
         |          |          |          |          |          |
FQEPVPKAAL HRHGRLSPRS AQARVTVEWL RVRDDGSNRT SLIDSRLVSV HESGWKAFDV

       190        200        210        220        230        240
         |          |          |          |          |          |
TEAVNFWQQL SRPRQPLLLQ VSVQREHLGP LASGAHKLVR FASQGAPAGL GEPQLELHTL

       250        260        270        280        290        300
         |          |          |          |          |          |
DLRDYGAQGD CDPEAPMTEG TRCCRQEMYI DLQGMKWAKN WVLEPPGFLA YECVGTCQQP

       310        320        330        340        350        360
         |          |          |          |          |          |
PEALAFNWPF LGPRQCIASE TASLPMIVSI KEGGRTRPQV VSLPNMRVQK CSCASDGALV

PRRLQP
```

O00292 in FASTA format

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Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.00 sec, SCORE=18430, Nseq=2, Len=366

unk|VIRT9911|Blast_submission  MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIP
sp|O75610|LFTB_HUMAN           MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIP
                               * **************.****** *************.***.*******:****

unk|VIRT9911|Blast_submission  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELV
sp|O75610|LFTB_HUMAN           YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELV
                               **.**:************************* **********************

unk|VIRT9911|Blast_submission  FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESG
sp|O75610|LFTB_HUMAN           FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESG
                               **********************:*********************************

unk|VIRT9911|Blast_submission  TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQ
sp|O75610|LFTB_HUMAN           TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQ
                               **************************************************

unk|VIRT9911|Blast_submission  DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECV
sp|O75610|LFTB_HUMAN           DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECV
                               ** ***********************************:***************

unk|VIRT9911|Blast_submission  PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA
sp|O75610|LFTB_HUMAN           PEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA
                               ******:************** ********************************

unk|VIRT9911|Blast_submission  PRRLQP
sp|O75610|LFTB_HUMAN           PRRLQP
                               ******
```

1: Ciba Found Symp. 1991;157:7-15; discussion 15-28.

Multiple forms of TGF-beta: distinct promote differential expression.

Roberts AB, Kim SJ, Noma T, Glick AB, Lafyatis R, Jakowlew SB, Geiser A, O'Reilly MA, Danielpour D,

Laboratory of Chemoprevention, National Cancer Instit MD 20892.

There are now five known distinct isoforms of TGF-beta identity. Of these, only TGF-beta 1, 2 and 3 thus far ha demonstrated to be expressed in mammalian tissues; TG been described only in chicken and TGF-beta 5 only in f the biological activities of these five isoforms of TGF-b indistinguishable in most in vitro assays their sites of sy localization in vivo are often distinct. Expression of the isoforms is differentially controlled both in vivo, as in d and in vitro after treatment of cells with steroids, such or tamoxifen, or with retinoids. To investigate the basis observations we have cloned and characterized the prom human TGF-beta 1, 2 and 3 genes. Significant differenc found: whereas the TGF-beta 1 promoter has no TATAA regulated principally by AP-1 sites, both the TGF-beta 2 promoters have TATAA boxes as well as AP-2 sites and

1: Mol Reprod Dev. 1995 Oct;42(2):131-40. Related

Transforming growth factor beta 1 expressior endometrium of the mare during placentation.

Lennard SN, Stewart F, Allen WR.

Thoroughbred Breeders' Association Equine Fertility U Paddocks, Suffolk, United Kingdom.

In situ hybridization, Northern blotting, and immunohist techniques were used to study the expression of transf factor beta 1 (TGF beta 1) in the endometrium of the m first 150 days of pregnancy (term = 330-340 days). In s hybridization using an oligonucleotide (45mer) probe, ba homologous region within all known mammalian TGF beta sequences, demonstrated TGF beta 1 mRNA accumulatio glandular and lumenal epithelial cells of the endometrium onwards which corresponds to the time of implantation Expression in the endometrium remained at a high level the sampling period (day 150). There was also marked ex TGF beta 1 in the mononuclear cells accumulated around of the specialized trophoblast cells of the endometrial endometrium and in the mononuclear cells accumulated i endometrial stroma of mares carrying failing donkey-in- pregnancies created by embryo transfer. The sense (co oligonucleotide probe exhibited no hybridization to any

stage. Northern blot analysis demonstrated that the oli probe and a porcine TGF beta 1 cDNA clone hybridized kb transcript in horse endometrial and lymphocyte RNA validating the oligonucleotide probe for detection of ho mRNA. Furthermore, both probes demonstrated an incr the pregnant endometrium from day 33 onwards, thereb the in situ hybridization results. Immunostaining with a anti-bovine TGF beta 1 serum also showed increasing TG accumulation in endometrial epithelia during pregnancy, of the protein in endometrial stroma and in the trophob the placenta after day 60 of pregnancy. These results s beta 1 expression increases in the maternal endometrium at the time of implantation and that it may play a role in endometrial and/or trophoblast growth and differentiat placentation in this species. It may also influence fetal (via placental transfer) at a later stage of gestation.

PMID: 8562058 [PubMed - indexed for MEDLINE]

1: Nature. 1996 May 9;381(6578):151-5. Related

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Related Resources

Comment in:

- Nature. 1996 May 9;381(6578):116-7.
- Nature. 1997 Jan 9;385(6612):111-2.

Left-right asymmetric expression of the TGF member lefty in mouse embryos.

Meno C, Saijoh Y, Fujii H, Ikeda M, Yokoyama T, Y Toyoda Y, Hamada H.

Tokyo Metropolitan Institute of Medical Science, Japan

Examples of lateral asymmetry are often found in verte the heart being on the left side, but the molecular mech governing the establishment of this left-right (L-R) han unknown. A diffusible morphogen may determine L-R pol likely molecule has not so far been identified. Here we r gene lefty, a member of the transforming growth facto which may encode a morphogen for L-R determination. L contains the cysteine-knot motif characteristic of this and is secreted as a processed form of relative molecul 25K-32K. Surprisingly, lefty is expressed in the left hal gastrulating mouse embryos. This asymmetric expressio transient and occurs just before the first sign of latera appears. In the mouse mutants iv and inv, which cause s

the sites of lefty expression are inverted, indicating th downstream of iv and inv. These results suggest that lef involved in setting up L-R asymmetry in the organ system

PMID: 8610011 [PubMed - indexed for MEDLINE]

Transforming growth factor beta 1 expression in the endometriu mare during placentation.

Lennard SN, Stewart F, Allen WR.

Thoroughbred Breeders' Association Equine Fertility Unit, Mertoun Paddock United Kingdom.

In situ hybridization, Northern blotting, and immunohistochemical technique study the expression of transforming growth factor beta 1 (TGF beta 1) in the of the mare during the first 150 days of pregnancy (term = 330-340 days). In hybridization using an oligonucleotide (45mer) probe, based on a homologou within all known mammalian TGF beta 1 DNA sequences, demonstrated TG mRNA accumulation in the glandular and lumenal epithelial cells of the endo from day 33 onwards which corresponds to the time of implantation (day 33- Expression in the endometrium remained at a high level to the end of the sam (day 150). There was also marked expression of TGF beta 1 in the mononucl accumulated around the periphery of the specialized trophoblast cells of the e cup within the endometrium and in the mononuclear cells accumulated in the stroma of mares carrying failing donkey-in-horse pregnancies created by eml The sense (control) oligonucleotide probe exhibited no hybridization to any t stage. Northern blot analysis demonstrated that the oligonucleotide probe and TGF beta 1 cDNA clone hybridized to a single 2.5 kb transcript in horse endo lymphocyte RNA, thus validating the oligonucleotide probe for detection of l beta 1 mRNA. Furthermore, both probes demonstrated an increased signal in endometrium from day 33 onwards, thereby confirming the in situ hybridizat Immunostaining with a specific anti-bovine TGF beta 1 serum also showed in TGF beta 1 accumulation in endometrial epithelia during pregnancy, and loca the protein in endometrial stroma and in the trophoblast layer of the placenta of pregnancy. These results show that TGF beta 1 expression increases in the endometrium of the mare at the time of implantation and that it may play a ro regulating endometrial and/or trophoblast growth and differentiation during p this species. It may also influence fetal development (via placental transfer) a of gestation.

PMID: 8562058 [PubMed - indexed for MEDLINE]

1: Hum Reprod. 1992 Oct;7(9):1214-21. Related

Entrez PubMed

Cytokine expression in human endometrium thr menstrual cycle.

Tabibzadeh S, Sun XZ.

Department of Pathology, University of South Florida H Center, Tampa 33612.

PubMed Services

Recent evidence suggests that diverse endometrial func regulated by cytokines. In this report, the presence of mRNA of cytokines were studied in human endometrium the menstrual cycle. The presence of the interleukin-1 (interleukin-1 (IL-1) beta, interleukin receptor antagonis interleukin-6 (IL-6) and transforming growth factor (TG proteins were demonstrated by immunohistochemical st IL-1 alpha and TGF-alpha proteins were strongly expres beta protein was weakly expressed in all the cells in the as epithelial cells. IRAP was markedly expressed in the morphological features of macrophages scattered in the the expression of IL-6 protein was predominant in the e epithelium. Diffuse cytoplasmic expression of IL-1 alpha endometrial epithelium during the proliferative phase co markedly with its enhanced luminal expression during th phase of the menstrual cycle. In addition, the presence of these cytokines in endometrium was established thro

Related Resources

entire menstrual cycle by reverse transcription-polymer reaction (RT-PCR). Abundant expression of cytokines in endometrium emphasizes the significant roles that cyto cell-cell interactions and in regulating endometrial funct

PMID: 1479000 [PubMed - indexed for MEDLINE]

09393628 PMID: 1353860

Correction: a new interpretation of a chicken transforming growth factor-beta 4 complementary DNA.

Burt D W ; Jakowlew S B

Department of Cellular and Molecular Biology, Edinburgh Research Station, Roslin, Midlothian, United Kingdom.

Molecular endocrinology (Baltimore, Md.) (UNITED STATES) Jun **1992** , 6 (6) p989-92, ISSN 0888-8809 Journal Code: 8801431

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Comparative Study

Descriptors: *Chickens--genetics--GE; *DNA--genetics--GE; *Protein Precursors--genetics--GE; *Transforming Growth Factor beta--genetics--GE; Amino Acid Sequence; Animals; Base Sequence; Molecular Sequence Data; Protein Sorting Signals--genetics--GE; Sequence Homology, Nucleic Acid; Species Specificity

Molecular Sequence Databank No.: GENBANK/X08012

CAS Registry No.: 0 (Protein Precursors); 0 (Protein Sorting Signals); 0 (Transforming Growth Factor beta); 110343-45-8 (transforming growth factor beta precursor); 9007-49-2 (DNA)

Record Date Created: 19920904

Record Date Completed: 19920904

1: Histochem Cell Biol. 1996 Jun;105(6):475-8. Related SpringerLink

Entrez PubMed

Immunochemical study of transforming growth in the kidney of the rat and chicken.

Diaz-Ruiz C, Montaner B, Perez-Tomas R.

Department de Biologia Cellular i Anatomia Putologica, L (Barcelona), Spain.

PubMed Services

Transforming growth factor-beta (TGF-beta) is a homo polypeptide of 25 kDa, which regulates cell growth and and influences extracellular matrix metabolism. Using im techniques, we identified TGF-beta in the loops of Henl collecting and Bellini ducts of rat kidney and in the loop chicken kidney. Furthermore, we detected two TGF-beta-immunoreactive proteins on kidney blots of th and 47 kDa, and three on chicken kidney blots of 12.5, 3 We suggest that the precursor forms of rat and chicke or beta 3, chicken TGF-beta 4, and the mature form of expressed in the collecting and Bellini ducts of rat kidne loops of Henle of rat and chicken kidney.

PMID: 8791107 [PubMed - indexed for MEDLINE]

Related Resources

1: Mol Endocrinol. 1992 Jun;6(6):989-92. Related

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Correction: a new interpretation of a chicken growth factor-beta 4 complementary DNA.

Burt DW, Jakowlew SB.

Department of Cellular and Molecular Biology, Edinburgh Station, Roslin, Midlothian, United Kingdom.

PMID: 1353860 [PubMed - indexed for MEDLINE]

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L3: Entry 1 of 8 File: USPT Nov 18, 2003

US-PAT-NO: 6649588
DOCUMENT-IDENTIFIER: US 6649588 B1

TITLE: Inhibition of TGF-.beta. and uses thereof

DATE-ISSUED: November 18, 2003

US-CL-CURRENT: 514/2; 514/21, 514/899, 530/350

INT-CL: [07] A61 K 38/00, A01 N 25/00, C07 K 17/00

L3: Entry 2 of 8 File: USPT Aug 6, 2002

US-PAT-NO: 6428966
DOCUMENT-IDENTIFIER: US 6428966 B1
**** See image for Certificate of Correction ****

TITLE: Growth differentiation factor, lefty-1

DATE-ISSUED: August 6, 2002

US-CL-CURRENT: 435/7.1; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7, 435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

L3: Entry 3 of 8 File: USPT Sep 25, 2001

US-PAT-NO: 6294662
DOCUMENT-IDENTIFIER: US 6294662 B1

TITLE: Nucleic acids encoding an endometrial bleeding associated factor (ebaf)

DATE-ISSUED: September 25, 2001

US-CL-CURRENT: 536/23.5; 435/6, 536/23.1, 536/24.31, 536/24.33

INT-CL: [07] C07 H 21/04, C12 Q 1/68

L3: Entry 4 of 8 File: USPT Jun 29, 1999

US-PAT-NO: 5916751
DOCUMENT-IDENTIFIER: US 5916751 A

TITLE: Method for the diagnosis of selected adenocarcinomas

DATE-ISSUED: June 29, 1999

US-CL-CURRENT: 435/6; 435/7.23, 436/64, 436/813

INT-CL: [06] G01 N 33/574, G01 N 33/48, C12 Q 1/68

L3: Entry 5 of 8 File: DWPI Nov 18, 2003

DERWENT-ACC-NO: 2002-352240
ABSTRACTED-PUB-NO: WO 200229105A

TITLE: Inhibiting the activity of transforming growth factor (TGF) beta, for treating e.g. fibrosis, comprises contacting tissue expressing TGF beta with ebaf peptide its analogue

INT-CL (IPC): A01 N 25/00, A01 N 37/18, A61 K 38/00, C07 K 1/00, C07 K 14/00, C07 K 17/00, C12 Q 1/68, G01 N 33/574
Derwent-CL (DC): B01, B04 , B05 , D16
CPI Codes: B04-E03F; B04-E08; B04-F11; B04-H06F; B04-N02; B14-F01; B14-F08; B14-G02D; B14-H01; B14-J05E; B14-L06; B14-N12; B14-N14; B14-N17A; B14-N17B; B14-S03; D05-H12A; D05-H12E; D05-H12F;

L3: Entry 6 of 8 File: DWPI Sep 25, 2001

DERWENT-ACC-NO: 2001-647266
ABSTRACTED-PUB-NO: US 6294662B

TITLE: New nucleic acid molecule encoding endometrial bleeding associated factor, useful in early diagnosis of selected adenocarcinomas in human, e.g. adenocarcinomas of colon, ovaries or testis

INT-CL (IPC): C07 H 21/04, C12 Q 1/68
Derwent-CL (DC): B04, D16
CPI Codes: B04-E03F; B04-E05; B11-C08E5; B12-K04A1; D05-H09; D05-H12A; D05-H12D1;

L3: Entry 7 of 8 File: DWPI Jun 29, 1999

DERWENT-ACC-NO: 1999-384717
ABSTRACTED-PUB-NO: US 5916751A

TITLE: Detecting serous or mucinous colon/ovarian adenocarcinomas and testicular adenocarcinoma by assaying for elevated expression of a gene

INT-CL (IPC): C12 Q 1/68, G01 N 33/48, G01 N 33/574
Derwent-CL (DC): B04, D16 , S03
CPI Codes: B04-B04C2; B04-B04L; B04-E01; B04-E05; B04-G02; B04-G21; B04-H01; B11-C07A; B11-C08E5; B12-K04A1; B12-K04F; D05-H09;
EPI Codes: S03-E14H1; S03-E14H4; S03-E14H6;

L3: Entry 8 of 8 File: DWPI Jan 30, 2003

DERWENT-ACC-NO: 1999-153704
ABSTRACTED-PUB-NO: US 6428966B

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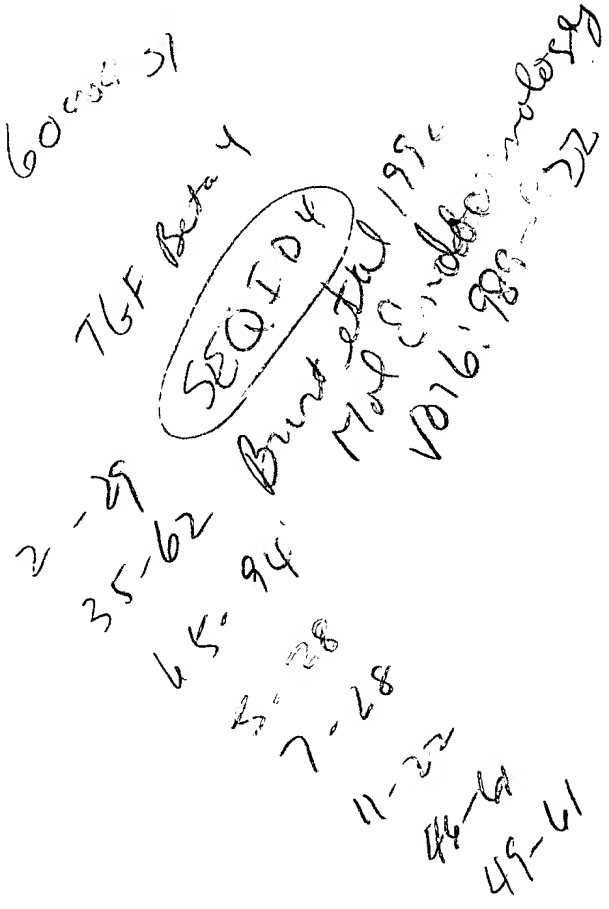
☐	L1	ebaf	134
☐	L2	('6683156')!.PN.	2
☐	L3	('US 5916751A' |'6428966' |'US 6747004B' |'6649588' |'6294662' |'5916751')!.PN.	8
☐	L4	endometrial near2 bleeding near associated	122
☐	L5	L4 not l1	14
☐	L6	('US 6683156B')!.PN.	0
☐	L7	('US 6683156B')!.PN.	0
☐	L8	TABIBZADEH.in.	21
☐	L9	6428966.pn.	2

END OF SEARCH HISTORY



L9: Entry 1 of 2 File: USPT Aug 6, 2002

US-PAT-NO: 6428966
DOCUMENT-IDENTIFIER: US 6428966 B1
**** See image for Certificate of Correction ****

TITLE: Growth differentiation factor, lefty-1

DATE-ISSUED: August 6, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lee; Se-Jin	Baltimore	MD		
Huynh; Thanh	Baltimore	MD		
Sebald; Suzanne	Jessup	MD		

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
The Johns Hopkins University School of Medicine	Baltimore	MD			02

APPL-NO: 09/ 485053 [PALM]
DATE FILED: January 31, 2000

PARENT-CASE:
This application is an application filed under 35 U.S.C. 371 from PCT/US98/15352, filed Jul. 24, 1998 which claims benefit from U.S. Provisional application 60/054,382 filed Jul. 31, 1997, both of which are incorporated by reference in their entirety.

PCT-DATA:

APPL-NO	DATE-FILED	PUB-NO	PUB-DATE	371-DATE	102(E)-DATE
PCT/US98/15352	July 24, 1998	WO99/06444	Feb 11, 1999	Mar 5, 2000	Mar 5, 2000

INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

US-CL-ISSUED: 435/7.1; 435/7.7, 435/7.9, 435/320.1, 435/325, 435/252.3, 435/254.11, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5
US-CL-CURRENT: 435/7.1; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7, 435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

FIELD-OF-SEARCH: 536/23.1, 536/23.5, 435/320.1, 435/325, 435/252.3, 435/7.1, 435/7.7, 435/7.9, 435/254.11, 530/387.1, 530/350, 530/387.9, 530/388.1, 530/388.23, 530/254.11, 530/388.24, 530/389.1, 530/389.2, 530/351

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected | Search ALL | Clear

	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5194596	March 1993	Tischer et al.	
☐	5350836	September 1994	Kopchick et al.	
☐	6027917	February 2000	Celeste et al.	

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ART-UNIT: 1646

PRIMARY-EXAMINER: Kemmerer; Elizabeth

ATTY-AGENT-FIRM: Gary Cary Ware & Freidenrich LLP Haile; Lisa A.

ABSTRACT:

Growth differentiation factor Lefty-1 polypeptide and polynucleotides are provided herein. Also disclosed are diagnostic and therapeutic methods of using the Lefty-1 polypeptide and polynucleotide sequences.

22 Claims, 1 Drawing figures

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#1	Search **1992 endocrinology burt**	09:48:02	0

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L2: Entry 1 of 2 File: USPT Jan 27, 2004

US-PAT-NO: 6683156
DOCUMENT-IDENTIFIER: US 6683156 B1
**** See image for Certificate of Correction ****

TITLE: Method for diagnosing selected adenocarcinomas

DATE-ISSUED: January 27, 2004

US-CL-CURRENT: 530/350; 530/351, 530/399, 536/23.1, 536/23.5

INT-CL: [07] C07 K 17/00, C07 H 21/04

L2: Entry 2 of 2 File: DWPI Jan 27, 2004

DERWENT-ACC-NO: 2004-118581
ABSTRACTED-PUB-NO: US 6683156B
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TITLE: New endometrial bleeding associated factor protein, useful for diagnosing a mucinous adenocarcinoma of the ovaries or colon in a female human or of the testis or colon of a male human

INT-CL (IPC): C07 H 21/04, C07 K 17/00
Derwent-CL (DC): B04, D16
CPI Codes: B04-C01G; B04-E03F; B04-N02A0E; B11-C08F4; B12-K04A1; D05-H09; D05-H12A;

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TITLE: A new growth differentiation factor, Lefty-1 - useful to detect and treat cell proliferative and immunological disorders

INT-CL (IPC): A61 K 38/18, C07 K 14/475, C07 K 16/22, C12 N 1/21, C12 N 5/06, C12 N 5/10, C12 N 15/12, C12 N 15/19, C12 N 15/63, C12 P 21/02, G01 N 33/48, G01 N 33/53
Derwent-CL (DC): B04, D16 , S03
CPI Codes: B04-C01; B04-E08; B04-F0100E; B04-G02; B04-H06; B12-K04A1; B12-K04A3; B14-G03; B14-H01; B14-H01B; B14-N17A; B14-P01; D05-H09; D05-H11; D05-H12A; D05-H12E; D05-H14; D05-H17A2;
EPI Codes: S03-E14H; S03-E14H4;

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Collections

Definition, Editing, Browsing

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US 6747004B
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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,621,919 sequences; 518,174,383 total letters

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	Db	AC	Description	Score	E-value
☐	sp	O00292	TGF4_HUMAN Transforming growth factor beta 4 precursor...	684	0.0
☐	sp	O75610	LFTB_HUMAN Left-right determination factor B precursor...	654	0.0
☐	tr	Q8BMF7	Mus musculus 13 days embryo male testis cDNA, RIKEN fu...	567	e-160
☐	sp	P57785	LFTB_MOUSE Left-right determination factor B precursor...	565	e-160
☐	sp	Q64280	TGF4_MOUSE Transforming growth factor beta 4 precursor...	556	e-157
☐	tr	Q9DFC6	TGF-beta family member lefty-A [Xenopus laevis (Africa...	232	7e-60
☐	tr	Q9DD36	Xantivin (Lefty-related factor Xatv) [Xantivin] [Xenop...	229	8e-59
☐	tr	Q9DFC5	TGF-beta family member lefty-B [Xenopus laevis (Africa...	228	1e-58
☐	tr	Q9PVN4	Lefty [Gallus gallus (Chicken)]	226	7e-58
☐	tr	Q9W6I7	Signaling molecule lefty2 [lft2] [Brachydanio rerio (Z...	219	5e-56

☐	tr	Q9PW55	Antivin [lft1] [Brachydanio rerio (Zebrafish) (Danio r...	219 5e-56
☐	tr	Q9PUK3	LEFTY-1 protein (Fragment) [LEFTY-1] [Gallus gallus (C...	218 1e-55
☐	tr	Q9W6I6	Signaling molecule lefty1 [lft1] [Brachydanio rerio (Z...	217 3e-55
☐	tr	Q95YK6	Lefty/antivin related protein [Cs-lfan] [Ciona savignyi]	145 1e-33
☐	tr	Q6T265	Antivin/lefty [Paracentrotus lividus (Common sea urchin)]	103 6e-21
☐	tr	Q767A1	Signaling molecule lefty1 (Fragment) [lefty1] [Oryzias...	84 4e-15
☐	tr	Q9XYQ7	Bone morphogenetic protein BMP2/4 [BMP2/4] [Lytechinus...	69 1e-10
☐	tr	Q8JIJ4	Bmp4 protein [Bmp4] [Steatocranus casuarius (lionhead ...	67 4e-10
☐	tr	Q8JIK1	Bmp4 protein [Bmp4] [Ctenochromis horei]	67 7e-10
☐	tr	Q78DH6	Bmp4 protein [Bmp4] [Gnathochromis permaxillaris]	66 9e-10
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☐	tr	Q78DH4	Bmp4 protein [Bmp4] [Ophthalmotilapia nasuta]	66 9e-10
☐	tr	Q78DH3	Bmp4 protein [Bmp4] [Tanganicodus irsacae (Spotfin gob...	66 9e-10
☐	tr	Q8JIK2	Bmp4 protein [Bmp4] [Astatoreochromis alluaudi (Alluau...	66 9e-10
☐	tr	Q8JIJ9	Bmp4 protein [Bmp4] [Haplochromis burtoni (Burton's mo...	66 9e-10
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☐	tr	Q8JIJ7	Bmp4 protein [Bmp4] [Julidochromis transcriptus]	66 1e-09
☐	tr	Q8JIJ3	Bmp4 protein [Bmp4] [Tropheus duboisi]	65 1e-09
☐	tr	Q90YJ3	Anti-dorsalizing morphogenetic protein [admp] [Brachyd...	65 2e-09
☐	tr	Q8JIK0	Bmp4 protein [Bmp4] [Cyprichromis leptosoma]	65 3e-09
☐	sp	P21275	BMP4_MOUSE Bone morphogenetic protein 4 precursor (BMP...	64 3e-09
☐	tr	Q8JIJ5	Bmp4 protein [Bmp4] [Oreochromis niloticus (Nile tilap...	64 3e-09
☐	tr	Q8UVQ2	Anti-dorsalizing morphogenetic protein [admp] [Brachyd...	64 6e-09
☐	tr	Q91597	Anti-dorsalizing morphogenetic protein 1 precursor [Xe...	63 7e-09
☐	tr	Q8UVQ8	Anti-dorsalizing morphogenetic protein [admp] [Brachyd...	63 7e-09
☐	tr	Q8JIJ8	Bmp4 protein [Bmp4] [Haplochromis nyererei]	63 7e-09
☐	sp	Q06826	BMP4_RAT Bone morphogenetic protein 4 precursor (BMP-4...	63 1e-08
☐	tr	Q811S3	Bone morphogenetic protein 4 [Bmp4] [Rattus norvegicus...	63 1e-08
☐	tr	Q6AYU9	Bmp4 protein [Bmp4] [Rattus norvegicus (Rat)]	63 1e-08
☐	tr	Q8AYB5	Bone morphogenetic protein 4 (Fragment) [Oryzias latip...	62 2e-08
☐	tr	P87380	Bone morphogenetic protein-4 (Fragment) [bmp4] [Brachy...	62 2e-08
☐	tr	O57574	Bone genetic protein 4 (Hypothetical protein) (Bone mo...	62 2e-08
☐	tr	Q6J3S5	Bone morphogenetic protein 24B [BMP24B] [Petromyzon ma...	61 3e-08
☐	tr	O13107	BMP4 [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)]	61 4e-08
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☐	sp	Q90752	BMP4_CHICK Bone morphogenetic protein 4 precursor (BMP...	60 5e-08
☐	sp	P25703	BMPA_XENLA Bone morphogenetic protein 2-I precursor (B...	59 1e-07
☐	tr	Q8MJV5	Bone morphogenetic protein 4 [sBmp4] [Suncus murinus (...	59 2e-07
☐	sp	P49001	BMP2_RAT Bone morphogenetic protein 2 precursor (BMP-2...	57 4e-07
☐	sp	P21274	BMP2_MOUSE Bone morphogenetic protein 2 precursor (BMP...	57 4e-07
☐	tr	Q90YD7	Bone morphogenetic protein 2 (BMP-2) [BMP-2] [Xenopus ...	57 4e-07
☐	tr	Q90YD6	Bone morphogenetic protein 4 [BMP-4] [Xenopus tropical...	57 4e-07
☐	tr	Q6PAF3	LOC397874 protein [LOC397874] [Xenopus laevis (African...	57 7e-07

☐	tr Q91703	Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (...	57	7e-07
☐	tr Q9MZV5	Bone morphogenetic protein 4 (Fragment) [bmp4] [Canis ...	57	7e-07
☐	sp P12644	BMP4_HUMAN Bone morphogenetic protein 4 precursor (BMP...	56	9e-07
☐	tr Q6J3S6	Bone morphogenetic protein 24A [BMP24A] [Petromyzon ma...	56	9e-07
☐	tr O73818	Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (...	56	9e-07
☐	tr Q9U418	Bone morphogenetic protein 2/4 [BMP2/4] [Branchiostoma...	56	1e-06
☐	sp O46576	BMP4_RABIT Bone morphogenetic protein 4 precursor (BMP...	55	2e-06
☐	sp P30885	BMP4_XENLA Bone morphogenetic protein 4 precursor (BMP...	55	2e-06
☐	tr Q90Y82	LjBmp2/4a (Fragment) [LjBmp2/4a] [Lampetra japonica (J...	55	2e-06
☐	tr O96504	Bone morphogenetic protein 2/4 [AmphiBMP2/4] [Branchio...	55	2e-06
☐	sp Q29607	BMP4_DAMDA Bone morphogenetic protein 4 precursor (BMP...	54	3e-06
☐	tr Q9U5E8	Pf-BMP2/4 [Pf-bmp2/4] [Ptychodera flava]	54	3e-06
☐	sp O46564	BMP2_RABIT Bone morphogenetic protein 2 precursor (BMP...	54	4e-06
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☐	tr Q9PVK1	Anti-dorsalizing morphogenetic protein [ADMP] [Gallus ...	54	4e-06
☐	sp P30884	BMPB_XENLA Bone morphogenetic protein 2-II precursor (...	53	8e-06
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☐	sp O08717	IHBE_MOUSE Inhibin beta E chain precursor (Activin bet...	53	1e-05
☐	sp P12643	BMP2_HUMAN Bone morphogenetic protein 2 precursor (BMP...	53	1e-05
☐	tr Q91XH3	Inhibin beta E [Inhbe] [Mus musculus (Mouse)]	53	1e-05
☐	tr Q7Q3Q7	AgCP11289 (Fragment) [agCG50272] [Anopheles gambiae st...	53	1e-05
☐	tr Q6PUC6	Decapentaplegic (Fragment) [Anopheles gambiae (African...	53	1e-05
☐	tr Q9W6T9	Activin beta B protein (Fragment) [inhbb] [Brachydanio...	52	2e-05
☐	tr Q9PWR8	Activin beta B subunit precursor [Carassius auratus (G...	52	2e-05
☐	tr Q869H8	GDF2 precursor [Crassostrea gigas (Pacific oyster)]	52	2e-05
☐	tr Q8MKC2	Bone morphogenetic protein 2 (Fragment) [Ovis aries (S...	52	2e-05
☐	tr Q8MXZ3	Bone morphogenetic protein [HpBMP] [Hemicentrotus pulc...	52	2e-05
☐	tr Q8IAE3	Sj-BMP2/4 [Sj-bmp2/4] [Stichopus japonicus (Sea cucumb...	51	3e-05
☐	tr Q6XDQ0	Bone morphogenetic protein 2 [Gallus gallus (Chicken)]	50	5e-05
☐	sp P27093	IHBB_CHICK Inhibin beta B chain precursor (Activin bet...	50	6e-05
☐	tr O13109	BMP2 [bmp2a] [Brachydanio rerio (Zebrafish) (Danio rer...	50	6e-05
☐	sp O88959	IHBE_RAT Inhibin beta E chain precursor (Activin beta-...	50	8e-05
☐	sp P17491	IHBB_RAT Inhibin beta B chain precursor (Activin beta-...	50	8e-05
☐	sp Q04999	IHBB_MOUSE Inhibin beta B chain precursor (Activin bet...	50	8e-05
☐	sp O95393	BM10_HUMAN Bone morphogenetic protein 10 precursor (BM...	50	8e-05
☐	sp P48969	DVR1_STRPU DVR-1 protein homolog precursor [DVR1] [Str...	49	1e-04
☐	tr Q90261	Activin beta B [inhbb] [Brachydanio rerio (Zebrafish) ...	49	1e-04
☐	tr Q869H7	GDF3 precursor (Fragment) [Crassostrea gigas (Pacific ...	49	1e-04
☐	sp P09529	IHBB_HUMAN Inhibin beta B chain precursor (Activin bet...	49	2e-04
☐	tr Q9PTF9	Bone morphogenetic protein 7 [bmp7] [Brachydanio rerio...	49	2e-04
☐	tr Q6EH35	Bone morphogenetic protein 2 (Fragment) [BMP-2] [Trach...	49	2e-04
☐	sp P58166	IHBE_HUMAN Inhibin beta E chain precursor (Activin bet...	48	2e-04
☐	sp Q9R229	BM10_MOUSE Bone morphogenetic protein 10 precursor (BM...	48	2e-04
☐	sp Q24735	60A_DROVI 60A protein precursor (Glass bottom boat pro...	48	2e-04
☐	tr Q9DGF1	Inhibin/activin (Fragment) [Cyprinus carpio (Common ca...	48	2e-04

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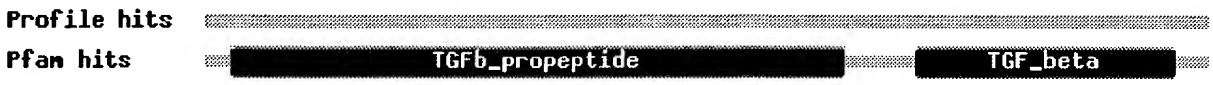

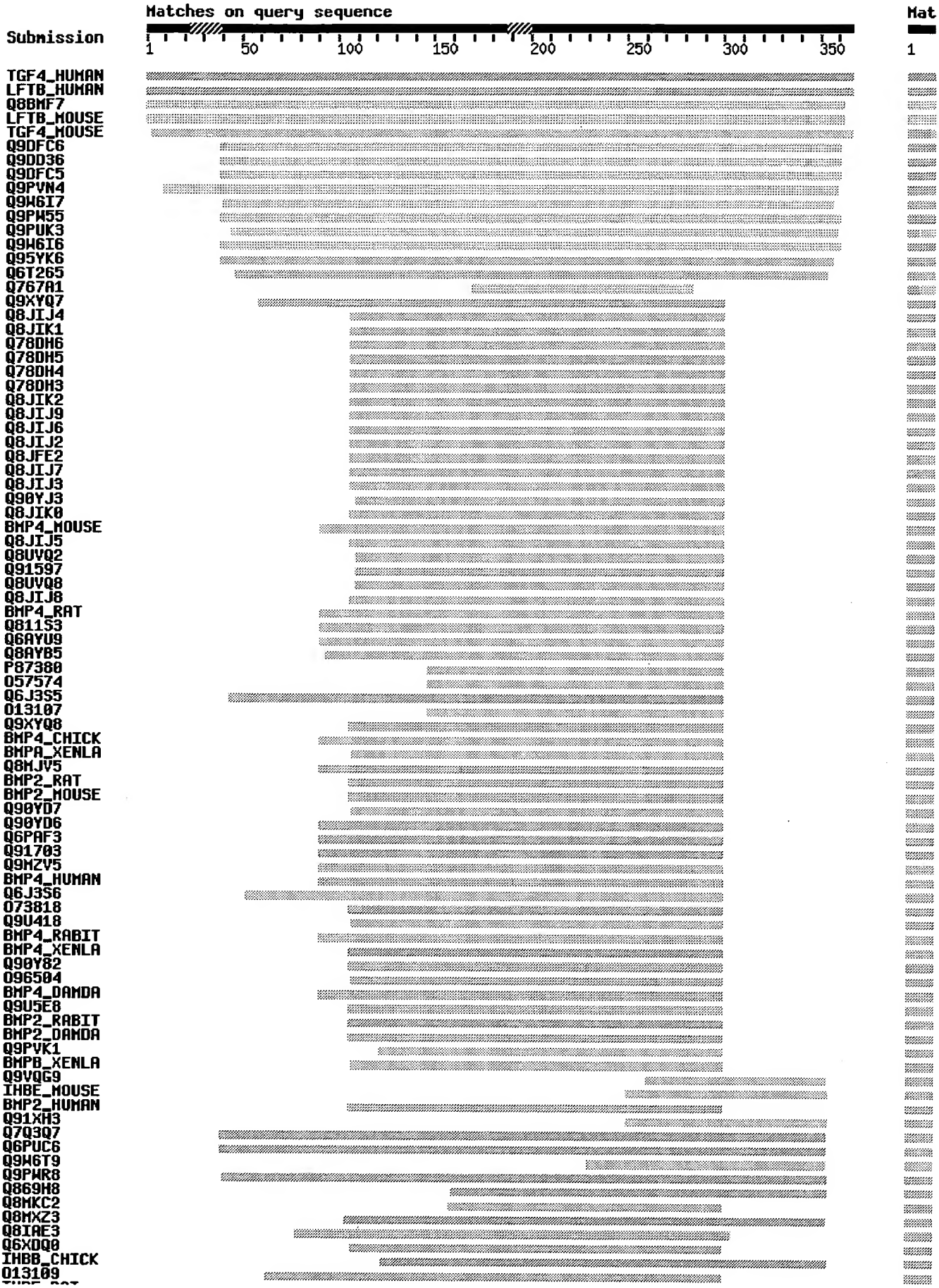
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BMP2_RABIT
BMP2_DAMDA
Q9PVK1
BMPB_XENLA
Q9VQG9
IHBE_MOUSE
BMP2_HUMAN
Q91XH3
Q7Q3Q7
Q6PUC6
Q9W6T9
Q9PWR8
Q869H8
Q8MKC2
Q8MXZ3
Q8IAE3
Q6XDQ0
IHBB_CHICK
O13109

Alignments

sp O00292 TGF4_HUMAN **Transforming growth factor beta 4 precursor (TGF-beta 4) (Endometrial bleeding-associated factor) (Left-right determination factor A) (Lefty-A protein) [EBAF] [Homo sapiens (Human)]** 366 AA align

Score = 684 bits (1765), Expect = 0.0
Identities = 337/366 (92%), Positives = 337/366 (92%)

```
Query: 1   MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQ 60
           MWPLWLCWALWVLPLAGPGAALT                VPVLDRADMEKLVIPAHVRAQ
Sbjct: 1   MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIPAHVRAQ 60

Query: 61  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
           YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL
Sbjct: 61  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180
           FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV
Sbjct: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240
           TEAVNFW             VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP
Sbjct: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV
Sbjct: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360

Query: 361 PRRLQP 366
           PRRLQP
Sbjct: 361 PRRLQP 366
```

sp O75610 LFTB_HUMAN **Left-right determination factor B precursor (Lefty-B protein) (UNQ278/PRO317) [LEFTB] [Homo sapiens (Human)]** 366 AA align

Score = 654 bits (1688), Expect = 0.0
Identities = 323/366 (88%), Positives = 328/366 (89%)

```
Query: 1   MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQ 60
           M PLWLCWALWVLPLA PGAALT                VP LDRADME+LVIP HVRAQ
Sbjct: 1   MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQ 60

Query: 61  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
           YV LL+RSHGDRSRGKRFSQSFREVAGRFLA EASTHLLVFGMEQRLPPNSELVQAVLRL
Sbjct: 61  YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180
```

```
            FQEPVPKAALHRHGRLSPRSA+ARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV
Sbjct: 121 FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240
            TEAVNFW              VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
            DL DYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWA+NWVLEPPGFLAYECVGTC+QP
Sbjct: 241 DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
            PEALAF WPFLGPRQCIASET SLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV
Sbjct: 301 PEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360

Query: 361 PRRLQP 366
            PRRLQP
Sbjct: 361 PRRLQP 366
```

tr Q8BMF7 **Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030463A22 product:LEFT-RIGHT DETERMINATION FACTOR B (LEFTY-2 PROTEIN), full insert sequence (Endometrial bleeding associated factor) [Ebaf] [Mus musculus (Mouse)]** 368 AA align

```
 Score =  567 bits (1461), Expect = e-160
 Identities = 274/364 (75%), Positives = 299/364 (81%), Gaps = 2/364 (0%)

Query: 1   MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQ 60
            M  LWLCWALWVLPLAGPGAA+T                  P LD AD+E++ IP HVR+Q
Sbjct: 1   MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIPTHVRSQ 60

Query: 61  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
            YV LL+ SH DRSRGKRFSQ+FREVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRL
Sbjct: 61  YVALLQGSHADRSRGKRFSQNFREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180
            FQEPVP+ AL R  RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV
Sbjct: 121 FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRTALIDSRLVSIHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLELH 238
            TEAVNFW              VSVQREHLGP    AHKLVRFA+QG P   G GEPQLELH
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGEPQLELH 240

Query: 239 TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ 298
            TLDL+DYGAQG+CDPE P+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C
Sbjct: 241 TLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCL 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGA 358
            Q PE+L   WPFLGPRQC+ASE  SLPMIVS+KEGGRTRPQVVSLPNMRVQ CSCASDGA
Sbjct: 301 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGA 360

Query: 359 LVPR 362
            L+PR
```

Sbjct: 361 LIPR 364

sp P57785 LFTB_MOUSE **Left-right determination factor B precursor (Lefty-2 protein) [Leftb] [Mus musculus (Mouse)]** 368 AA align

Score = 565 bits (1455), Expect = e-160
Identities = 273/364 (75%), Positives = 298/364 (81%), Gaps = 2/364 (0%)

```
Query: 1   MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQ 60
           M  LWLCWALWVLPLAGPGAA+T                    P LD AD+E++ IP HVR+Q
Sbjct: 1   MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIPTHVRSQ 60

Query: 61  YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
           YV LL+ SH DRSRGKRFSQ+ REVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRL
Sbjct: 61  YVALLQGSHADRSRGKRFSQNLREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180
           FQEPVP+ AL R  RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV
Sbjct: 121 FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRTALIDSRLVSIHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLELH 238
           TEAVNFW              VSVQREHLGP    AHKLVRFA+QG P   G GEPQLELH
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGEPQLELH 240

Query: 239 TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ 298
           TLDL+DYGAQG+CDPE P+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C
Sbjct: 241 TLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCL 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGA 358
           Q PE+L   WPFLGPRQC+ASE  SLPMIVS+KEGGRTRPQVVSLPNMRVQ CSCASDGA
Sbjct: 301 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGA 360

Query: 359 LVPR 362
           L+PR
Sbjct: 361 LIPR 364
```

sp Q64280 TGF4_MOUSE **Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty protein) (Lefty-1 protein) (STRA3 protein) [Ebaf] [Mus musculus (Mouse)]** 368 AA align

Score = 556 bits (1432), Expect = e-157
Identities = 271/365 (74%), Positives = 295/365 (80%), Gaps = 2/365 (0%)

```
Query: 4   LWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQYVV 63
           LWLCWALW L L     ALT                  PVLD+AD+E +VIP+HVR QYV
Sbjct: 4   LWLCWALWALSLVSLREALTGEQILGSLLQQLQLDQPPVLDKADVEGMVIPSHVRTQYVA 63

Query: 64  LLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQE 123
           LL+ SH  RSRGKRFSQ+ REVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRLFQE
Sbjct: 64  LLQHSHASRSRGKRFSQNLREVAGRFLVSETSTHLLVFGMEQRLPPNSELVQAVLRLFQE 123
```

```
Query: 124 PVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEA 183
           PVP+ AL R  RLSP SA+ARVT+EWLR RDDGSNRT+LIDSRLVS+HESGWKAFDVTEA
Sbjct: 124 PVPRTALRRQKRLSPHSARARVTIEWLRFRDDGSNRTALIDSRLVSIHESGWKAFDVTEA 183

Query: 184 VNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLELHTLD 241
           VNFW              VSVQREHLGP    +HKLVRFA+QG P   G GEPQLELHTLD
Sbjct: 184 VNFWQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQGTPDGKGQGEPQLELHTLD 243

Query: 242 LRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPP 301
           L+DYGAQG+CDPEAP+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C Q P
Sbjct: 244 LKDYGAQGNCDPEAPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCLQLP 303

Query: 302 EALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVP 361
           E+L   WPFLGPRQC+ASE  SLPMIVS+KEGGRTRPQVVSLPNMRVQ CSCASDGAL+P
Sbjct: 304 ESLTSRWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGALIP 363

Query: 362 RRLQP 366
           RRLQP
Sbjct: 364 RRLQP 368
```

tr Q9DFC6 **TGF-beta family member lefty-A [Xenopus laevis (African clawed frog)]** 366 AA

align

```
 Score =  232 bits (592), Expect = 7e-60
 Identities = 126/330 (38%), Positives = 193/330 (58%), Gaps = 16/330 (4%)

Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK--------RFSQSFREVAGRFLA 91
           VP L++ D+E LVIP H++A+Y+ +L  SH +R R           R      +++G  L
Sbjct: 43  VPKLEKRDVENLVIPRHIQAKYMSMLH-SHRERKRRSLPSLAGILRGISGNADISGEILY 101

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLR 151
           S++S   +VFGME R+P NSE+  A L+LF++P PK       R      + ARV+V ++
Sbjct: 102 SDSSKQTMVFGMESRIPENSEVTMAELKLFKKP-PKIMNVPERRFHRPVSNARVSVYYVE 160

Query: 152 VRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPL 211
           +  DG+NRTSL+DSRLV + ESGW++FDVT+AV++W               + V  E  G
Sbjct: 161 ILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MKSGGHSSMHLEIHVDGERHGSH 219

Query: 212 ASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYI 270
           AS   K+VRF +Q  +   LG+P+L L TL+L ++GA+GDC       +   CCR+E +I
Sbjct: 220 ASEMAKMVRFTTQSPSDNSLGKPELVLFTLNLDEHGARGDCSASGAKKDNI-CCREEYFI 278

Query: 271 DLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPMIVSI 330
           + + + W + W++EP G+ A+ C G+C+QP   L+ ++   G R C   E+A LP++  +
Sbjct: 279 NFRELTWTQYWIIEPAGYNAFRCAGSCKQPKYPLSHHY---GERMCAVVESAPLPVMYLV 335

Query: 331 KEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           K+G  T  +V    PNM V+KC C  D   +
Sbjct: 336 KKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 365
```

tr Q9DD36 **Xantivin (Lefty-related factor Xatv) [Xantivin] [Xenopus laevis** 367 AA

(African clawed frog)] align

Score = 229 bits (583), Expect = 8e-59
Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

```
Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFR----------EVAGRF 89
           VP L++ D+E LVIP H++A+Y+ +L   H  R R KR   S            +++G
Sbjct: 43  VPKLEKRDVENLVIPGHIQAKYMSML---HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90  LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP-----VPKAALHRHGRLSPRSAQAR 144
           L S++S   LVFGME R+P NSE+  A L+LF++P     VP+   HR          AR
Sbjct: 100 LYSDSSKQSLVFGMESRIPENSEVTMAELKLFKKPPKIMNVPERRFHRPVN------NAR 153

Query: 145 VTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQ 204
           V+V ++ +  DG+NRTSL+DSRLV + ESGW++FDVT+AV++W             + V
Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPLASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRC 263
            E  G  AS   K+VRF +Q  +   LG+P+L L TL+L + G +GDC       +   C
Sbjct: 213 GERHGSHASEMAKMVRFTTQSPSDNSLGKPELVLFTLNLNEQGTRGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETAS 323
           CR+E +I+ + + + W + W++EP G+ A+ C G+C+QP   L+      G R C   E+A
Sbjct: 272 CREEYFINFRELTWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESAP 329

Query: 324 LPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           LP++  +K+G  T  +V   PNM V+KC C  D   +
Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 366
```

tr Q9DFC5 **TGF-beta family member lefty-B [Xenopus laevis (African clawed frog)]** 367 AA

align

Score = 228 bits (582), Expect = 1e-58
Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

```
Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFR----------EVAGRF 89
           VP L++ D+E LVIP H++A+Y+ +L   H  R R KR   S            +++G
Sbjct: 43  VPKLEKRDVENLVIPRHIQAKYMSML---HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90  LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP-----VPKAALHRHGRLSPRSAQAR 144
           L S++S   LVFGME R+P NSE+  A L+LF++P     VP+   HR          AR
Sbjct: 100 LYSDSSKQSLVFGMESRIPENSEVTMAELKLFKKPPKIMNVPERRFHRPVN------NAR 153

Query: 145 VTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQ 204
           V+V ++ +  DG+NRTSL+DSRLV + ESGW++FDVT+AV++W             + V
Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWRSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPLASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRC 263
            E  G  AS   K+VRF +Q  +   LG+P+L L TL+L + G +GDC       +   C
Sbjct: 213 GERHGSHASEMAKMVRFTTQSPSDNSLGKPELVLFTLNLNEQGTRGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETAS 323
           CR+E +I+ + + + W + W++EP G+ A+ C G+C+QP   L+      G R C   E+A
Sbjct: 272 CREEYFINFRELTWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESAP 329
```

```
Query: 324 LPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           LP++  +K+G  T  +V   PNM V+KC C  D   +
Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 366
```

tr Q9PVN4 **Lefty [Gallus gallus (Chicken)]** 362 AA align

```
 Score =  226 bits (575), Expect = 7e-58
 Identities = 131/352 (37%), Positives = 187/352 (52%), Gaps = 8/352 (2%)

Query: 10  LWVLPLAGPGAALTXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQYVVLLRRSH 69
           L+VL L     A T                 VP L + D+  LVIP HV+ +Y+ +L+R
Sbjct: 9   LYVLCLVAMACAFTQEGFKEVMLKQLGLSEVPKLHKRDLVDLVIPEHVKNKYISMLKRHR 68

Query: 70  GDRSRGKRFSQSFREVAGR--FLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPK 127
           G R       +   + + G      S+      +F ME R+P NSE+  A L+LF++P+ +
Sbjct: 69  GKRRASPSLASILQGIPGNAEVFYSDPMRQNFIFDMEGRIPKNSEVTMAELKLFKKPLDR 128

Query: 128 AALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFW 187
             L       P S  ARV++ W++ + DG+NRTSLIDSRLV + ESGWK FDVT+AV++W
Sbjct: 129 VNLPARQPHRPVS-NARVSIYWVQRQHDGTNRTSLIDSRLVPIRESGWKNFDVTQAVHYW 187

Query: 188 XXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGA-PAGLGEPQLELHTLDLRDYG 246
                    V ++ E +   A+   K VRF SQ A    +G P+L L+TLDL DYG
Sbjct: 188 -LRNKRQEPMVLQVWIEGERVASYAAEVAKSVRFTSQDAGDRAVGRPELVLYTLDLEDYG 246

Query: 247 AQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAF 306
             GDC       + T CCRQ+ YI+ + + W + WV+EP G+ AY C G C Q P  L
Sbjct: 247 GPGDCKDGVQAGKST-CCRQKHYINFRELSWTQYWVIEPAGYQAYSCRGGCLQLPGPLQL 305

Query: 307 NWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGA 358
            W     R C  +E++ LP++  ++ G  T  +     PNM ++KCSC +DGA
Sbjct: 306 -WGG-RERACAVAESSPLPIMYLVRRGNHTEIEATEFPNMIIEKCSCMADGA 355
```

tr Q9W6I7 **Signaling molecule lefty2 [lft2] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 362 AA align

```
 Score =  219 bits (559), Expect = 5e-56
 Identities = 121/330 (36%), Positives = 183/330 (54%), Gaps = 25/330 (7%)

Query: 41  PVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK-------RFSQSFREVAGRFLASE 93
           P + + D+E LV+PAH++++Y+ +L+  H  R R          R       ++ G    S+
Sbjct: 39  PRIQKRDLENLVVPAHIKSKYLSMLKLHHQRRRRSLPSLAGILRGIHGNADITGEIKYSD 98

Query: 94  ASTHLLVFGMEQRLPPNSELVQAVLRLFQEPV--PKAALHRHGRLSPRSAQARVTVEWLR 151
            +   LVF ME RL  N+E+  A L+LFQ     P      RH R        ARV++ W+
Sbjct: 99  TTRQRLVFDMEARLQENTEVTMAELKLFQTAAQSPSKPERRHHR---PINHARVSIYWVE 155

Query: 152 VRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPL 211
           V ++GSNRTSL+DSRLV +HESGW++FDVT+A+++W              V  + E  G
Sbjct: 156 VLENGSNRTSLLDSRLVPIHESGWRSFDVTQAIHYW-SKSQKKAPLHLEVWTEGERPGSY 214
```

```
Query: 212 ASGAHKLVRFASQGAPAG-----LGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQ 266
           A+   K VRFA+Q          +G P+L L+TLDL +YG+QG+C+         ++CCR+
Sbjct: 215 AAEMAKRVRFATQDPKENTLEKDMGAPELVLYTLDLDEYGSQGNCNSS---PNSSKCCRE 271

Query: 267 EMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPM 326
           E +I+ + + W + W++EP G+ A+ C G C+QP       +   G R C   E+A LPM
Sbjct: 272 EHFINFRELTWTQYWIIEPAGYQAFRCAGGCKQPKR----GFYGYGQRTCAVMESAPLPM 327

Query: 327 IVSIKEGGRTRPQVVSLPNMRVQKCSCASD 356
           +  +K+G  T  +V    PNM V+KC C+ D
Sbjct: 328 MYLVKKGDYTEIEVAEFPNMIVEKCGCSMD 357
```

tr Q9PW55 **Antivin [lft1] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 358 AA

align

```
 Score =  219 bits (559), Expect = 5e-56
 Identities = 115/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK-------RFSQSFREVAGRFLAS 92
           +P + + D+E LVIP HV+ +Y+ +L+  H  + R          R       +++G F+ S
Sbjct: 39  IPQIHKRDLENLVIPTHVKNKYISMLKLHHSRKRRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93  EASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRV 152
           + +   +VF M  R+P NSE+  A L+L+++   K ++       P +  ARV++ W+
Sbjct: 99  DTTRQRVVFEMTSRIPENSEVTMAELKLYKKAPHKRSIPERKGHRPVN-NARVSIYWVEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLA 212
           + DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W              V ++ E  G  A
Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFDVTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFASQGAPAG-LGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271
           +   K V F +Q      LG+P+L L+TL+L ++G+ GDC+      +   CCR++ +I+
Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEEFGSSGDCENN---KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331
            + + W + W++EP G+ A+ C G C+QP     +     G R+C   E+A LPM+  +K
Sbjct: 274 FRALTWTQYWIIEPSGYQAFRCKGGCRQPKRNYGY-----GERKCAVVESAPLPMMYLVK 328

Query: 332 EGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           +G  T  +V    PNM V+KC C  D   V
Sbjct: 329 KGDYTEIEVAEFPNMIVEKCGCAMDNISV 357
```

tr Q9PUK3 **LEFTY-1 protein (Fragment) [LEFTY-1] [Gallus gallus (Chicken)]** 320 AA

align

```
 Score =  218 bits (556), Expect = 1e-55
 Identities = 122/317 (38%), Positives = 177/317 (55%), Gaps = 8/317 (2%)

Query: 45  RADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFREVAGR--FLASEASTHLLVFG 102
           + D+  LVIP HV+ +Y+ +L+R  G R       +   + + G      S+       +F
Sbjct: 2   KRDLVDLVIPEHVKNKYISMLKRHRGKRRASPSLASILQGIPGNAEVFYSDPMRQNFIFD 61
```

```
Query: 103 MEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSL 162
           ME R+P NSE+  A L+LF++P+ +  L       P S  ARV++ W++ + DG+NRTSL
Sbjct: 62  MEGRIPKNSEVTMAELKLFKKPLDRVNLPARQPHRPVS-NARVSIYWVQRQHDGTNRTSL 120

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFA 222
           IDSRLV + ESGWK FDVT+AV++W             V ++ E +   A+   K VRF
Sbjct: 121 IDSRLVPIRESGWKNFDVTQAVHYW-LRNKRQEPMVLQVWIEGERVASYAAEVAKSVRFT 179

Query: 223 SQGA-PAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNW 281
           SQ A    +G P+L L+TLDL DYG  GDC       + T CCRQ+ YI+ + + W + W
Sbjct: 180 SQDAGDRAVGRPELVLYTLDLEDYGGPGDCKDGVQAGKST-CCRQKHYINFRELSWTQYW 238

Query: 282 VLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVV 341
           V+EP G+ AY C G C Q P  L   W     R C  +E++ LP++  ++ G  T  +
Sbjct: 239 VIEPAGYQAYSCRGGCLQLPGPLQL-WGG-RERACAVAESSPLPIMYLVRRGNHTEIEAT 296

Query: 342 SLPNMRVQKCSCASDGA 358
             PNM ++KCSC +DGA
Sbjct: 297 EFPNMIIEKCSCMADGA 313
```

tr Q9W6I6 **Signaling molecule lefty1 [lft1] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 358 AA align

```
 Score =  217 bits (552), Expect = 3e-55
 Identities = 114/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK-------RFSQSFREVAGRFLAS 92
           +P + + D+E LVIP +V+ +Y+ +L+  H  + R          R       +++G F+ S
Sbjct: 39  IPQIHKRDLENLVIPTNVKNKYISMLKLHHSRKRRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93  EASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRV 152
           + +   +VF M  R+P NSE+  A L+L+++   K ++       P +  ARV++ W+
Sbjct: 99  DTTRQRVVFEMTSRIPENSEVTMAELKLYKKAPHKRSIPERKGHRPVN-NARVSIYWVEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLA 212
           + DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W              V ++ E  G  A
Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFDVTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFASQGAPAG-LGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271
           +   K V F +Q      LG+P+L L+TL+L ++G+ GDC+      +   CCR++ +I+
Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEEFGSSGDCENN---KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331
            + + W + W++EP G+ A+ C G C+QP     +     G R+C   E+A LPM+  +K
Sbjct: 274 FRALTWTQYWIIEPSGYQAFRCKGGCRQPKRNYGY-----GERKCAVVESAPLPMMYLVK 328

Query: 332 EGGRTRPQVVSLPNMRVQKCSCASDGALV 360
           +G  T  +V   PNM V+KC CA D   V
Sbjct: 329 KGDYTEIEVAEFPNMIVEKCGCAMDNISV 357
```

tr Q95YK6 **Lefty/antivin related protein [Cs-lfan] [Ciona** 372 AA

savignyi] align

```
 Score =  145 bits (366), Expect = 1e-33
 Identities = 107/348 (30%), Positives = 160/348 (45%), Gaps = 43/348 (12%)

Query: 40  VPVLDRADMEKLVIPAHVRAQYVVLLRR-SHGDRSRGKRFSQS-FREV------AGRFLA 91
           VP     ++  +VIP   R +Y  ++ + +  +R+R     Q  FR V       G  +
Sbjct: 32  VPRFTHNEVRNVVIPDETRRKYERMVEKMTKLERNRRSSSLQDLFRSVHKKTGIEGDVIY 91

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRL--------------- 136
           S+     L F ME RLP +  +  A LRLF++      L  H R+
Sbjct: 92  SDTFREELKFDMEGRLPDDYMISMAELRLFKK------LPNHNRILSRLRTPSGNRNDVQ 145

Query: 137 --SPRSAQ-----ARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXX 189
             S R  Q     ARV++       DG   T L+DSRL+ V+ SGW  FDVT A+  W
Sbjct: 146 LSSARGRQQVIRNARVSIHLSLPLPDGGAVTELVDSRLILVNGSGWHTFDVTSAIRKWRR 205

Query: 190 XXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQ 248
                    + VQ    G  A+   +L+RF  Q  A       P+L ++T + ++
Sbjct: 206 HPVRYMTITLELKVQSSSPGRAAAELARLIRFTGQRVALDSPRRPELVVYT-NAKEPART 264

Query: 249 GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNW 308
            DC       +  +CCR+  +++ +  KW+K+W+LEP GF AY C G C+ ,     +
Sbjct: 265 SDCSSSRHNRQH-KCCRENRFVNFRETKWSKHWILEPAGFNAYHCAGGCRSDRRRNSKG- 322

Query: 309 PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASD 356
              PR C A+ET SLP++  +K+GG     +V    PNM ++KCSCA D
Sbjct: 323 ---APRSCSATETNSLPIMYLVKKGGAIHVEVSEFPNMVIEKCSCALD 367
```

tr Q6T265 **Antivin/lefty [Paracentrotus lividus (Common sea urchin)]** 404 AA

align

```
 Score =  103 bits (256), Expect = 6e-21
 Identities = 89/359 (24%), Positives = 138/359 (37%), Gaps = 60/359 (16%)

Query: 47  DMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQR 106
           D   L +P H+R QY  + R+    R+   +      E+ G    +E +  L  F +
Sbjct: 52  DASTLTVPDHLRFQYESMHRQHRVRRAYITKGIHKNEEIYGEVSYTERNRQLFTFDISS- 110

Query: 107 LPPNSELVQAVLRLFQE--------------PVPKAALHRHGRLSPRSAQARVT------ 146
           +P  SE++ A L++++E                P +  H H   +  S +  V
Sbjct: 111 IPEGSEVIMAELKVYKERPNHSIFKPEGEEGEAPHSNNHDHVHSALVSIKQLVDQEVDMD 170

Query: 147 VEWLRVRDDGSNR-----TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV 201
            E   + D+  N+     T  ID R +++  +GWK FDVT  +  W
Sbjct: 171 AEPADLADEVVNQHDGMDTITIDQREMTLKGAGWKVFDVTNTIQTWVADSDSNLGVAL-- 228

Query: 202 SVQREHLGPLASGAHKL-----VRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAP 256
               H+ P+  G H        + FA+   P     P      +      A    +P
Sbjct: 229 -----HIDPIEGGHHAQQVVDEMVFATDFFPETPDSPDSRPVLVIYTTKYAPASDEPNEC 283

Query: 257 MTEGT---RCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEAL---AFNWPF 310
            EG    RCCR+  Y+D + + W   W++EP GF A++C G C  P         F  PF
Sbjct: 284 RYEGEEEHRCCRRRKYVDFRDLSWTSRWIIEPAGFEAFDCYGPCHNPRSRHIRDVFRLPF 343
```

```
Query: 311 LGP---------------RQCIASETASLPMI-VSIKEGGRTRPQVVSLPNMRVQKCSC 353
           G                R C  S ++SLPM+ +S    G    +V  +PNM V+ C C
Sbjct: 344 FGASSSGSSIFGAGSGGHRTCGVSRSSSLPMMYLSETPSGTVELKVEEIPNMIVEDCGC 402
```

tr Q767A1 **Signaling molecule lefty1 (Fragment) [lefty1] [Oryzias latipes (Medaka fish) (Japanese ricefish)]** 112 AA

align

```
 Score = 84.0 bits (206), Expect = 4e-15
 Identities = 41/115 (35%), Positives = 66/115 (56%), Gaps = 5/115 (4%)

Query: 170 VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAG 229
           +HE+GWK+FDVT+AV++W             V ++ E  G  A+   K VRF +Q
Sbjct: 2   IHETGWKSFDVTQAVHYW-SKTQQKTPMHLEVWIEGERPGSYAAEVAKSVRFTTQEQTEH 60

Query: 230 L-GEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVL 283
             G+P+L L+TL+L +YG++GDCD          CCR++ +ID + + W + W++
Sbjct: 61  TSGKPELVLYTLNLEEYGSRGDCD---VYQSKDTCCREQYFIDFRALTWTQYWII 112
```

tr Q9XYQ7 **Bone morphogenetic protein BMP2/4 [BMP2/4] [Lytechinus variegatus (Sea urchin)]** 417 AA

align

```
 Score = 69.3 bits (168), Expect = 1e-10
 Identities = 70/280 (25%), Positives = 110/280 (39%), Gaps = 47/280 (16%)

Query: 60  QYVVLLRRSHGDRSRGKRFSQSF---------------REVAGRFLASEASTHLLVFGME 104
           QY++ L RSH +   G      F                 E AG+ L +E    H ++F +
Sbjct: 81  QYMMDLYRSHTEHQDGISMHFDFDHLSTGTANTIRSYHHEDAGQVLPTEHHRHTVIFNIS 140

Query: 105 QRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSA------QARVTVEWLRVRDDGSN 158
             +P    L  A LRLF++ + + ++ +   L  R +        R+ V  + ++    N
Sbjct: 141 T-MPAEEVLTMAELRLFRKDLEEHSIAKRHALDDRKSLEPIHYMQRINVFHI-LKPVARN 198

Query: 159 RTS---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGA 215
           R +   LID+RLV V  S W++FDV  AV  W              +  R    P
Sbjct: 199 RDTIKRLIDTRLVDVRNSSWESFDVRPAVTSWVEVPEKNHGLEIELIDSRGRPSP----N 254

Query: 216 HKLVRFASQGAPAGLGEPQLELHTL------DLRDYGAQGDCDPEAPMTEGTR------- 262
           H  VR   +  P+ + E Q E           +  Y   G     +P + G +
Sbjct: 255 HHHVRVTREADPSKVQELQNEEDERWFQTRPQIVTYSDDGR-TKRSPSSRGRKRKGKRLK 313

Query: 263 --CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             C R  +Y+D    + W  +W++ P G+ AY C G C  P
Sbjct: 314 ANCRRHPLYVDFSDVHW-NDWIVAPAGYQAYYCHGECPFP 352
```

tr Q8JIJ4 **Bmp4 protein [Bmp4] [Steatocranus casuarius (lionhead cichlid)]** 403 AA

align

```
 Score = 67.4 bits (163), Expect = 4e-10
 Identities = 60/205 (29%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+DS
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDS 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   + P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIK1 **Bmp4 protein [Bmp4] [Ctenochromis horei]** 403 AA
align

```
 Score = 66.6 bits (161), Expect = 7e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+DS
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   + P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWKQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q78DH6 **Bmp4 protein [Bmp4] [Gnathochromis permaxillaris]** 403 AA
align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+DS
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   + P   G H  +  +
```

```
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P        +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q78DH5 **Bmp4 protein [Bmp4] [Haplotaxodon microlepis]** 403 AA
align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P        +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q78DH4 **Bmp4 protein [Bmp4] [Ophthalmotilapia nasuta]** 403 AA
align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P        +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q78DH3 **Bmp4 protein [Bmp4] [Tanganicodus irsacae (Spotfin goby cichlid)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIK2 **Bmp4 protein [Bmp4] [Astatoreochromis alluaudi (Alluaud's haplo)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVGHNVSRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIJ9 **Bmp4 protein [Bmp4] [Haplochromis burtoni (Burton's mouthbrooder)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIJ6 **Bmp4 protein [Bmp4] [Labidochromis caeruleus (blue streak hap)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--ARERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIJ2 **Bmp4 protein [Bmp4] [Tilapia rendalli (redbreast tilapia)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201
```

```
Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--THERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JFE2 **Bmp4 protein [Bmp4] [Boulengerochromis microlepis (Giant cichlid)]** 403 AA align

```
 Score = 66.2 bits (160), Expect = 9e-10
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIJ7 **Bmp4 protein [Bmp4] [Julidochromis transcriptus]** 403 AA align

```
 Score = 65.9 bits (159), Expect = 1e-09
 Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPVDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315
```

```
Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
           W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8JIJ3 **Bmp4 protein [Bmp4] [Tropheus duboisi]** 403 AA
align

```
 Score = 65.5 bits (158), Expect = 1e-09
 Identities = 59/205 (28%), Positives = 87/205 (41%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV    S W++FDV+ AV  W             V V   +  P   G H  +  +
Sbjct: 202 RLVRHDASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
           W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q90YJ3 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA
align

```
 Score = 65.1 bits (157), Expect = 2e-09
 Identities = 63/231 (27%), Positives = 92/231 (39%), Gaps = 63/231 (27%)

Query: 110 NSELVQAVLRLFQ-EPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTS----LID 164
           + +++ A L LF+  P     L+RH              V   +V D G    S    L+
Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNRHHFCQ---------VSVYQVLDSGKKNVSQGKKLLS 168

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLAS-----GAH--- 216
           SRLV +H +GW+ F +T+AV  W              +S +  +LG L S     G+
Sbjct: 169 SRLVPIHSTGWEVFTITQAVRSW-------------MSDEGSNLGLLVSVRTLAGSQMDL 215

Query: 217 KLVRFASQGAPAGLGEPQLELHTLD------LRDYGAQGDCDPEAPMT------------ 258
           K+VRFAS         +P L L T D      L       D  P +P
Sbjct: 216 KMVRFASGRDHHHSKQPMLVLFTDDGRRAASLEATSKGSDVSPGSPSQPLPSVPASRRSP 275

Query: 259 ---------EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                  E   C RQ +Y+D + + W+  W++ P G+ AY C G+C  P
Sbjct: 276 RSVDYDERGEKMACQRQPLYVDFEEIGWS-GWIVSPKGYNAYHCKGSCIFP 325
```

tr Q8JIK0 **Bmp4 protein [Bmp4] [Cyprichromis leptosoma]** 403 AA

align

Score = 64.7 bits (156), Expect = 3e-09
Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S      R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQXLHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W             V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGQHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G   P       +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
           W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

sp P21275 BMP4_MOUSE **Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B) [Bmp4] [Mus musculus (Mouse)]** 408 AA align

Score = 64.3 bits (155), Expect = 3e-09
Identities = 59/226 (26%), Positives = 87/226 (38%), Gaps = 32/226 (14%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE+S   +F +   +P N  +  A LRLF+E V +         HR          A +
Sbjct: 134 SESSAFRFLFNLSS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEMV 192

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W              + V
Sbjct: 193 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLEL-------HTLDLRDYGAQGDCDPE 254
           H      G H  +   S+  P G G+     P L          HTL  R          P+
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQGSGDWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
               +   C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 300 RSRKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344
```

tr Q8JIJ5 **Bmp4 protein [Bmp4] [Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)]** 403 AA align

Score = 64.3 bits (155), Expect = 3e-09
Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S      R+ V E L+    G   T L+D+
```

```
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISHDQGLHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGTR----CCRQEMYIDLQGM 275
             P  GE  +L  L L +G  G   P         +P  G +     C R  +Y+D    +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q8UVQ2 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA align

```
 Score = 63.5 bits (153), Expect = 6e-09
 Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

Query: 110 NSELVQAVLRLFQ-EPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLV 168
           + +++ A L LF+  P     L+RH          Q  V         + + S     L+ SRLV
Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNRH-----HFCQVSVYQVLDSSKKNVSQGKKLLSSRLV 172

Query: 169 SVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLAS-----GAH---KLVR 220
            +H +GW+ F +T+AV  W             +S +  +LG L S     G+    K+VR
Sbjct: 173 PIHSTGWEVFTITQAVRSW-------------MSDEGSNLGLLVSVRTLAGSQMDLKMVR 219

Query: 221 FASQGAPAGLGEPQLELHTLDLR------------DYGAQGDCDPEAPMTEGTR------ 262
           FAS         +P L LT D R            D  G  P  +  R
Sbjct: 220 FASGRDHHHSKQPMLVLFTDDGRRAASLEATSKGSDVSPGGSSQPLPSVPASRRSSRSVD 279

Query: 263 ---------CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                    C RQ +Y+D + + W+  W++ P G+ AY C G+C  P
Sbjct: 280 YDERGEKMACQRQPLYVDFEEIGWS-GWIVSPKGYNAYHCKGSCIFP 325
```

tr Q91597 **Anti-dorsalizing morphogenetic protein 1 precursor [Xenopus laevis (African clawed frog)]** 390 AA align

```
 Score = 63.2 bits (152), Expect = 7e-09
 Identities = 56/217 (25%), Positives = 86/217 (38%), Gaps = 38/217 (17%)

Query: 110 NSELVQAVLRLFQ---EPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSR 166
           N +++ A L LF+     P +A    RH        Q  V +    + +         L+ S+
Sbjct: 120 NEKILTAELHLFKLKPRPSEQAYFKRH-----HFCQISVYMVLDKNKIQLPQGRKLLSSK 174

Query: 167 LVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGA 226
           LV +H SGW+ F +T+AV  W                 ++      + P          ++RFAS
Sbjct: 175 LVPIHSSGWEVFSITQAVRAWNDESANHGILVTVRNLGGAQVDP------NIIRFASGRD 228

Query: 227 PAGLGEPQLELHTLDLR----DYGAQGDCD-------PEAPMTEGTR------------C 263
```

```
              +P L L T D R        Q D         P AP +  TR            C
Sbjct: 229 HHESKQPMLVLFTDDGRRGIVSVNNQPDDQLMPLPNVPMAPTSNRTRLGRSVEEDGQLPC 288

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
            R  +Y+D + + W+  W++ P G+ AY C G+C  P
Sbjct: 289 QRHPLYVDFEEIGWS-GWIISPRGYNAYHCKGSCPFP 324
```

tr Q8UVQ8 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA align

```
 Score = 63.2 bits (152), Expect = 7e-09
 Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

Query: 110 NSELVQAVLRLFQ-EPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLV 168
           + +++ A L LF+  P     L+RH        Q  V       + + S    L+ SRLV
Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNRH-----HFCQVSVYQVLDSSKKNVSQGKKLLSSRLV 172

Query: 169 SVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLAS-----GAH---KLVR 220
            +H +GW+ F +T+AV  W             +S +  +LG L S     G+    K+VR
Sbjct: 173 PIHSTGWEVFTITQAVRSW-------------MSDEGSNLGLLVSVRTLAGSQMDLKMVR 219

Query: 221 FASQGAPAGLGEPQLELHTLDLR------------DYGAQGDCDPEAPMTEGTR------ 262
           FAS        +P L L T D R            D    G   P   +    R
Sbjct: 220 FASGRDHHHSKQPMLVLFTDDGRRAASLEATSKGSDVSPGGXSQPLPSVPASRRSSRSVD 279

Query: 263 ---------CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                  C RQ +Y+D + + W+  W++ P G+ AY C G+C  P
Sbjct: 280 YDERGEKMACQRQPLYVDFEEIGWS-GWIVSPKGYNAYHCKGSCIFP 325
```

tr Q8JIJ8 **Bmp4 protein [Bmp4] [Haplochromis nyererei]** 403 AA align

```
 Score = 63.2 bits (152), Expect = 7e-09
 Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
           +P +  L  A LRL++  + +A       +S   A  R+ V E L+    G   T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           RLV  + S W++FDV+ AV  W              V V   +  P   G H  +  +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--ARERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGD------CDPEAPMTEGTR----CCRQEMYIDLQGM 275
            P   GE   +L  L L  +G  G           +P   G +    C R  +Y+D   +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHSLTRRTKRSPRQRGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr Q811S3 **Bone morphogenetic protein 4 [Bmp4] [Rattus norvegicus (Rat)]** 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08
Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE+S     F +   +P N  +  A LRLF+E V +        HR          A +
Sbjct: 134 SESSAFRFFFNLSS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEMV 192

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W             + V
Sbjct: 193 --------PGHLITRLLDTRLVRHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-------HTLDLRDYGAQGDCDPE 254
           H      G H  +   S+  P G G      P L         HTL  R         P+
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQGSGNWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
               +   C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 300 RSRKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344
```

tr Q6AYU9 **Bmp4 protein [Bmp4] [Rattus norvegicus (Rat)]** 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08
Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE+S     F +   +P N  +  A LRLF+E V +        HR          A +
Sbjct: 134 SESSAFRFFFNLSS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEMV 192

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W             + V
Sbjct: 193 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-------HTLDLRDYGAQGDCDPE 254
           H      G H  +   S+  P G G      P L         HTL  R         P+
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQGSGNWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
               +   C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 300 RSRKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344
```

tr Q8AYB5 **Bone morphogenetic protein 4 (Fragment) [Oryzias latipes (Medaka fish) (Japanese ricefish)]** 392 AA

align

Score = 62.0 bits (149), Expect = 2e-08
Identities = 58/216 (26%), Positives = 92/216 (41%), Gaps = 19/216 (8%)

```
Query: 95  STHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRD 154
           S HL         +P +  L  A LRL+++ + +A  +    L+ +         E L+
Sbjct: 133 SIHLRFLFNLSSIPEDELLSSAELRLYRQQLGEA--NDDSPLNDQGLHRINIYEVLKPPR 190

Query: 155 DGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASG 214
            G   T L+D+RLV  + S W++FDV+ AV  W              ++V+  HL
Sbjct: 191 PGQLITQLLDTRLVHHNASRWESFDVSPAVLRW----TRERLPNYGLAVEILHLNQTPHN 246

Query: 215 AHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGD------CDPEAPMTEGTR----CC 264
            H+ VR  S+      GE   ++  L L  +G  G           +P   G +    C
Sbjct: 247 QHRHVRI-SRSLHQEPGEDWDQVRPL-LVTFGHDGKGHSLTRRTKRSPKPRGRKRNRNCR 304

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           R  +Y+D   + W  +W++ PPG+ AY C G C  P
Sbjct: 305 RHTLYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 339
```

tr P87380 **Bone morphogenetic protein-4 (Fragment) [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA align

```
 Score = 61.6 bits (148), Expect = 2e-08
 Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREH 207
           E L+   +G   T L+D+RLV  + S W++FDV+ AV  W              V V +
Sbjct: 180 EVLKAPREGQLITQLLDTRLVRHNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 237

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGT 261
             P+  G H  V  +    P    E   +L  L L  +G  G   P          +P   G
Sbjct: 238 RNPVQKGRHVRVSRSVHPLP---DEEWDQLRPL-LVTFGHDGKSHPLTRRAKRSPKQRGR 293

Query: 262 R----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +    C R  +Y+D   + W  +W++ PPG+ AY C G C  P
Sbjct: 294 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 335
```

tr O57574 **Bone genetic protein 4 (Hypothetical protein) (Bone morphogenetic protein 4) [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 400 AA align

```
 Score = 61.6 bits (148), Expect = 2e-08
 Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREH 207
           E L+   +G   T L+D+RLV  + S W++FDV+ AV  W              V V +
Sbjct: 181 EVLKAPREGQLITQLLDTRLVRHNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 238

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGT 261
             P+  G H  V  +    P    E   +L  L L  +G  G   P          +P   G
Sbjct: 239 RNPVQKGRHVRVSRSVHPLP---DEEWDQLRPL-LVTFGHDGKSHPLTRRAKRSPKQRGR 294

Query: 262 R----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +    C R  +Y+D   + W  +W++ PPG+ AY C G C  P
```

```
Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 336
```

tr Q6J3S5 **Bone morphogenetic protein 24B [BMP24B] [Petromyzon marinus (Sea lamprey)]** 451 AA align

```
 Score = 61.2 bits (147), Expect = 3e-08
 Identities = 67/287 (23%), Positives = 109/287 (37%), Gaps = 33/287 (11%)

Query: 45  RADMEKLV---IPAHVRAQYVVLLRRSHGDRS--RGKRFSQSFREVAGRFLASEASTHLL 99
           RAD E++    +      + V   R + G  +  RG    +S  +++       + +T
Sbjct: 103 RADKERVGKDDVDVEEEKEEVAFPREAQGRANTVRGFHHDESTEKLSLGQSTEDGTTWHF 162

Query: 100 VFGMEQRLPPNSELVQAVLRLFQEPV--PKAALHRHGRLSPRSAQARVTVEWLRVRDDGS 157
           +F +   +P + E+  A LR+    V  P  +      L+PR  +  V
Sbjct: 163 LFNLSS-IPDSEEVTAAELRVHHTRVHSPCPSSSPACELAPRLERINVYEVVAPPSSPSG 221

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV-SVQREHLGPLASGAH 216
             + L+D+R+V  +ES W+AFDV+ AV+ W              V  V+R   G  A+G
Sbjct: 222 AASRLLDTRVVRTNESRWEAFDVSPAVSRWTRGSAPNRGFAVEVLPVRRPSGGVAANGVP 281

Query: 217 KLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTR-------------- 262
               A   +      P    H  + R        D  AP T  +R
Sbjct: 282 SEAVLAQPRSGVASLFPGDGSHQTEPRPLLVTFGSDGRAPFTPRSRARRSIGGAPRQAAH 341

Query: 263 ---------CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                  C R  +Y+D + + W  +W++ PPG+ AY C G C  P
Sbjct: 342 KARRKPRYSCRRHALYVDFREVGW-NDWIVAPPGYHAYFCHGECPFP 387
```

tr O13107 **BMP4 [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 400 AA

align

```
 Score = 60.8 bits (146), Expect = 4e-08
 Identities = 47/163 (28%), Positives = 69/163 (41%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREH 207
           E L+   +G   T L+D+RLV  + S W++FDV+ AV  W              V V +
Sbjct: 181 EVLKAPREGQLITQLLDTRLVRPNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 238

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGT 261
             P+  G H  V  +    P    E    + L L  +G  G   P      +P   G
Sbjct: 239 RNPVQKGRHARVSRSVHPLP---NEEWDHVRPL-LVTFGHDGKSHPLTRRAKRSPKQRGR 294

Query: 262 R----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +    C R  +Y+D   + W  +W++ PPG+ AY C G C  P
Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECPFP 336
```

tr Q9XYQ8 **Bone morphogenetic protein BMP2/4 (Fragment) [BMP2/4] [Strongylocentrotus purpuratus (Purple sea urchin)]** 289 AA align

```
 Score = 60.8 bits (146), Expect = 4e-08
 Identities = 57/222 (25%), Positives = 88/222 (38%), Gaps = 34/222 (15%)

Query: 107 LPPNSELVQAVLRLFQEP------VPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT 160
           +P    +  A LRLF++       V + ALH    L P     R+ V  + ++    NR
Sbjct: 7   MPEEEVMTTAELRLFRKDLDEHHIVKRHALHDRESLKPIHYMQRINVYHI-LKPVARNRD 65

Query: 161 S---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHK 217
           +   LID+RLV V  + W++FDV  A+  W             +   R    P     H
Sbjct: 66  TIKRLIDTRLVDVRNASWESFDVRPAMRVWLEEPEKNHGLEIELIDSRGRPSP----NHH 121

Query: 218 LVRFASQGAPAGLGE-------------PQLELHTLDLRDYGAQGDCDP--EAPMTEGTR 262
            VR   +  P+ + E              PQ+  ++ D R   +             +G R
Sbjct: 122 HVRVTREADPSKVEELENEEEDRWFQTRPQIVTYSDDGRTKRSPSSSSSGRGQKKRKGKR 181

Query: 263 ----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
               C R E+Y+D   + W  +W++ P G+ AY C G C  P
Sbjct: 182 LKANCRRHELYVDFSDVHW-NDWIVAPAGYQAYYCRGECPFP 222
```

sp Q90752 BMP4_CHICK **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4] [Gallus gallus (Chicken)]** 405 AA align

```
 Score = 60.5 bits (145), Expect = 5e-08
 Identities = 62/224 (27%), Positives = 93/224 (40%), Gaps = 31/224 (13%)

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPV--PKAALHRHGRLSPRSAQARVTV-E 148
           SEA     VF +   +P N  +    LRL++E V  P AA  R           R+ + E
Sbjct: 134 SEAPRIRFVFNLSS-VPDNEVISSEELRLYREQVEEPSAAWERGFH--------RINIYE 184

Query: 149 WLRVRDDGSNR-TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREH 207
            ++   + S   T L+D+RLV  + + W+ FDV+ AV  W              + V   H
Sbjct: 185 VMKPLSERSQAITRLLDTRLVHHNVTRWETFDVSPAVIRW--TKDKQPNHGLVIEVTHLH 242

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP------EAPMTEGT 261
                G H  +   S+  P G G     +L  L L  +G  G           +P   G+
Sbjct: 243 QAQTHQGKHVRI---SRSLPQGHGGDWAQLRPL-LVTFGHDGRGHALTRRARRSPKHHGS 298

Query: 262 R-----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           R     C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 299 RKNKKNCRRHALYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 341
```

sp P25703 BMPA_XENLA **Bone morphogenetic protein 2-I precursor (BMP-2-I) [Xenopus laevis (African clawed frog)]** 398 AA align

```
 Score = 59.3 bits (142), Expect = 1e-07
 Identities = 59/210 (28%), Positives = 89/210 (42%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLFQEPVPK------AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158
           PN ELV  A LR+F+E V +       + LHR    +  + P +A +R  V
Sbjct: 142 PNEELVTSAELRIFREQVQEPFESDSSKLHRINIYDIVKPAAAASRGPV---------- 190
```

```
Query: 159 RTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218
           L+D+RLV  +ES W++FDVT A+  W                V+  HL    +   K
Sbjct: 191 -VRLLDTRLVHHNESKWESFDVTPAIARWIAHKQPNHGFV----VEVNHLDNDKNVPKKH 245

Query: 219 VRFASQGAPAGLGEPQ----LELHTLDLRDYGAQGDCDPEAPMTEGTR----CCRQEMYI 270
           VR +    P     PQ    L   + D + +        +A   +  R    C R  +Y+
Sbjct: 246 VRISRSLTPDKDNWPQIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLYV 305

Query: 271 DLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 306 DFSDVGW-NDWIVAPPGYHAFYCHGECPFP 334
```

tr Q8MJV5 **Bone morphogenetic protein 4 [sBmp4] [Suncus murinus (House shrew) (Musk shrew)]** 409 AA align

```
 Score = 58.5 bits (140), Expect = 2e-07
 Identities = 58/227 (25%), Positives = 84/227 (36%), Gaps = 33/227 (14%)

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE S     F +   +P N  +  A LRLF+E V +         HR           A V
Sbjct: 134 SENSAFRFFFNLSS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEVV 192

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W              + V
Sbjct: 193 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG--------AQGDCDP 253
           H      G H  +   S+  P G G+     P L     D R +                P
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQGNGDWAQLRPLLVTFGHDGRGHALTRRRRAKRSPKHHP 299

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +   +   C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 300 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 345
```

sp P49001 BMP2_RAT **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) [Bmp2] [Rattus norvegicus (Rat)]** 393 AA align

```
 Score = 57.4 bits (137), Expect = 4e-07
 Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNR---TSLI 163
           +P +  L  A L++F+E + +A       L   S Q R+ + +      S++   T L+
Sbjct: 137 VPTDEFLTSAELQIFREQMQEA-------LGNSSFQHRINIYEIIKPATASSKFPVTRLL 189

Query: 164 DSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVS-------VQREHLGPLASGAH 216
           D+RLV+ + S W++FDVT AV  W              V+       V + H+  ++   H
Sbjct: 190 DTRLVTQNTSQWESFDVTPAVMRWTAQGHTNHGFVVEVAHLEEKPGVSKRHV-RISRSLH 248

Query: 217 KLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMY 269
           +     SQ  P         G G P   LH  + R           +      + C R  +Y
Sbjct: 249 QDEHSWSQVRPLLVTFGHDGKGHP---LHKREKR------QAKHKQRKRLKSSCKRHPLY 299
```

```
Query: 270 IDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +D    + W   +W++ PPG+ A+ C G C   P
Sbjct: 300 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 329
```

sp P21274 BMP2_MOUSE **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) [Bmp2] [Mus musculus (Mouse)]** 394 AA align

```
 Score = 57.4 bits (137), Expect = 4e-07
 Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNR----TSL 162
           +P +  L  A L++F+E + +A       L   S Q R+ +  + ++   +N     T L
Sbjct: 138 VPSDEFLTSAELQIFREQIQEA-------LGNSSFQHRINIYEI-IKPAAANLKFPVTRL 189

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLG------PLASGAH 216
           +D+RLV+ + S W++FDVT AV  W              V+   E+ G       ++   H
Sbjct: 190 LDTRLVNQNTSQWESFDVTPAVMRWTTQGHTNHGFVVEVAHLEENPGVSKRHVRISRSLH 249

Query: 217 KLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMY 269
           +     SQ  P        G G P   LH  + R           +      + C R  +Y
Sbjct: 250 QDEHSWSQIRPLLVTFGHDGKGHP---LHKREKR------QAKHKQRKRLKSSCKRHPLY 300

Query: 270 IDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +D    + W   +W++ PPG+ A+ C G C   P
Sbjct: 301 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 330
```

tr Q90YD7 **Bone morphogenetic protein 2 (BMP-2) [BMP-2] [Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)]** 398 AA align

```
 Score = 57.4 bits (137), Expect = 4e-07
 Identities = 57/210 (27%), Positives = 88/210 (41%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLFQEPVPK------AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158
           PN ELV   A LR+F+E V +       + LHR    +  + P +A +R  V
Sbjct: 142 PNEELVTSAELRIFREGVQEPFEGDSSKLHRINIYDIVKPAAAASRGPV---------- 190

Query: 159 RTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218
              L+D+RL+  +ES W++FDVT A+  W              V+    HL    +   K
Sbjct: 191 -VRLLDTRLIHHNESKWESFDVTPAITRWIAHKQPNHGFVVEVT----HLDNDKNVPKKH 245

Query: 219 VRFASQGAPAGLG----EPQLELHTLDLRDYGAQGDCDPEAPMTEGTR----CCRQEMYI 270
           VR +    P         P L   + D + +        +A   +  R    C R  +Y+
Sbjct: 246 VRISRSLVPDKDSWPRIRPLLVTFSHDGKGHALHKREKRQARHKQRKRLKSSCRRHPLYV 305

Query: 271 DLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           D    + W   +W++ PPG+ A+ C G C   P
Sbjct: 306 DFSDVGW-NDWIVAPPGYHAFYCHGECPFP 334
```

tr Q90YD6 **Bone morphogenetic protein 4 [BMP-4] [Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)]** 400 AA align

Score = 57.4 bits (137), Expect = 4e-07
Identities = 49/220 (22%), Positives = 90/220 (40%), Gaps = 24/220 (10%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHG--RLSPRSAQARVTVEW 149
           +E      VF +   +P N  +  A LRL++E +        G  R++       +T
Sbjct: 130 AENGNFRFVFNLSS-IPENEVISSAELRLYREQIDHGPAWEEGFHRINIYEVMKPITAS- 187

Query: 150 LRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLG 209
                G   + L+D+RL+  + + W++FDV+ A+  W             ++++  HL
Sbjct: 188 ------GHMISRLLDTRLIHHNVTQWESFDVSPAIIRWTRDKQINHG----LAIEVVHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG----AQGDCDPEAPMTEG 260
              +   K VR +    P    +     P L   + D R +     ++      + P  +
Sbjct: 238 QTKTYQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 298 KHCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336
```

tr Q6PAF3 **LOC397874 protein [LOC397874] [Xenopus laevis (African clawed frog)]** 400 AA align

Score = 56.6 bits (135), Expect = 7e-07
Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHG--RLSPRSAQARVTVEW 149
           +E      VF +   +P N  +  A LRL++E +        G  R++       +
Sbjct: 130 AENGNFRFVFNLSS-IPENEVISSAELRLYREQIDHGPAWDEGFHRINIYEVMKPIAANG 188

Query: 150 LRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLG 209
           L +     NR  L+D+RL+  + + W++FDV+ A+  W             ++++  HL
Sbjct: 189 LMI-----NR--LLDTRLIHHNVTQWESFDVSPAIMRWTRDKQINHG----LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG----AQGDCDPEAPMTEG 260
              +   K VR +    P    +     P L   + D R +     ++      + P  +
Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 298 KHCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336
```

tr Q91703 **Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African clawed frog)]** 400 AA align

Score = 56.6 bits (135), Expect = 7e-07
Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHG--RLSPRSAQARVTVEW 149
           +E      VF +   +P N  +  A LRL++E +        G  R++       +
Sbjct: 130 AENGNFRFVFNLSS-IPENEVISSAELRLYREQIDHGPAWDEGFHRINIYEVMKPIAANG 188

Query: 150 LRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLG 209
           L +     NR  L+D+RL+  + + W++FDV+ A+  W             ++++  HL
Sbjct: 189 LMI-----NR--LLDTRLIHHNVTQWESFDVSPAIMRWTRDKQINHG----LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG----AQGDCDPEAPMTEG 260
              +   K VR +    P    +     P L   + D R +     ++     + P  +
Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 298 KHCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336
```

tr Q9MZV5 **Bone morphogenetic protein 4 (Fragment) [bmp4] [Canis familiaris (Dog)]** 337 AA align

```
 Score = 56.6 bits (135), Expect = 7e-07
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPK-----AALHRHGRLSPRSAQARVT 146
           SE S    +F +   +P N  +  A LRLF+E V +         HR          A V
Sbjct: 62  SENSAFRFLFNLSS-IPENEVISSAELRLFREQVNQDPDWEQGFHRINIYEVMKPPAEVV 120

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W             + V
Sbjct: 121 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 170

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLEL-------HTLDLRDYGAQG-DCDP 253
           H      G H  +   S+  P G G+     P L         H L  R    +
Sbjct: 171 HQTRTHQGQHVRI---SRSLPQGSGDWAQLRPLLVTFGHDGRGHALTRRQRAKRSPKHHA 227

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +   +   C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 228 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 273
```

sp P12644 BMP4_HUMAN **Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B) [BMP4] [Homo sapiens (Human)]** 408 AA align

```
 Score = 56.2 bits (134), Expect = 9e-07
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE S    +F +   +P N  +  A LRLF+E V +         HR          A V
Sbjct: 133 SENSAFRFLFNLSS-IPENEVISSAELRLFREQVDQGPDWERGFHRINIYEVMKPPAEVV 191

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W             + V
Sbjct: 192 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 241
```

```
Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLELHTLDLRDYG----AQGDCDP---- 253
           H      G H  +   S+  P G G      P L     D R +      +    P
Sbjct: 242 HQTRTHQGQHVRI---SRSLPQGSGNWAQLRPLLVTFGHDGRGHALTRRRRAKRSPKHHS 298

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +    +   C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 299 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344
```

tr Q6J3S6 **Bone morphogenetic protein 24A [BMP24A] [Petromyzon marinus (Sea lamprey)]** 422 AA align

Score = 56.2 bits (134), Expect = 9e-07
Identities = 81/291 (27%), Positives = 114/291 (38%), Gaps = 50/291 (17%)

```
Query: 54  PAHVRAQYVVLLRRS-HGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGME--QRLPPN 110
           P  V   Y++ L R+ HG  S  +   +    +  R  AS+A+T       E  + +P +
Sbjct: 74  PGAVVPPYMLQLYRALHGAHSGARDVGRPLDRLVAR-PASQANTVRSFHHDESAEHVPAD 132

Query: 111 SELVQAVLRLFQ-------EPVPKAALH--RHGRLSPRSAQA-RVTV-EWLR-VRDDGSN 158
           S    A   LF        E +  A LH  R    SP SA   R+ V E LR    DG+
Sbjct: 133 SGDSTARRLLFNVSSIPDGEVITSAELHVYRERLSSPASAGLHRINVYEVLRPAAADGTP 192

Query: 159 RTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218
              L+D+R+V    S W+ FDV+ A   W             + V+ +HL        +
Sbjct: 193 IARLLDTRVVHSGRSEWERFDVSPAAVRWAATKEPNHG----LLVEVQHLDGGTPEKRRH 248

Query: 219 VRF----------------ASQGAPAGLGEPQLEL------HTLDLRDYGAQGDCDPEA- 255
           VR                AS+G   G G PQL        H    RD G      P+
Sbjct: 249 VRIGRSLHAEAVAAAARDGASEGGDGGEGWPQLRPLLVTFGHDGKTRDEGTLLRPRPKRN 308

Query: 256 --PMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             P   G R    C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 309 SRPNKGGRRGRGQCARYPLYVDFSDVGW-NDWIVAPPGYNAFFCQGECHFP 358
```

tr O73818 **Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African clawed frog)]** 400 AA align

Score = 56.2 bits (134), Expect = 9e-07
Identities = 47/205 (22%), Positives = 86/205 (41%), Gaps = 23/205 (11%)

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHG--RLSPRSAQARVTVEWLRVRDDGSNRTSLID 164
           +P N  +  A LRL++E +        G  R++       +    L +     NR  L+D
Sbjct: 144 IPENEVISSAELRLYREQIDHGPAWDEGFHRINIYEVMKPIAANGLMI-----NR--LLD 196

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQ 224
           +RL+  + + W++FDV+ A+  W             ++++  HL    +   K VR +
Sbjct: 197 TRLIHHNVTQWESFDVSPAIMRWTRDKQINHG----LAIEVIHLNQTKTHQGKHVRISRS 252

Query: 225 GAPAGLGE-----PQLELHTLDLRDYG----AQGDCDPEAPMTEGTRCCRQEMYIDLQGM 275
             P    +     P L   + D R +     ++     + P  +   C R  +Y+D   +
```

```
Sbjct: 253 LLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKNKHCRRHSLYVDFSDV 312

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
           W  +W++ PPG+ A+ C G C  P
Sbjct: 313 GW-NDWIVAPPGYQAFYCHGDCPFP 336
```

tr Q9U418 **Bone morphogenetic protein 2/4 [BMP2/4] [Branchiostoma belcheri (Amphoxius)]** 411 AA align

```
 Score = 55.8 bits (133), Expect = 1e-06
 Identities = 54/206 (26%), Positives = 83/206 (40%), Gaps = 18/206 (8%)

Query: 109 PNSELVQAV-LRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRV--RDDGSNRTSLIDS 165
           P+ EL++A  LRLF+E +    + ++G  +          E +R   R +    T L+D+
Sbjct: 145 PSVELIKAAELRLFREQIDVDHV-QYGDSTDHHLYRVNVYEVMRPNSRTNTDTITRLLDT 203

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           +LV V  S W++FDV  AV  W             V V     G L++   +L R
Sbjct: 204 KLVDVRNSSWESFDVRSAVTKWKNSPERNYGLE--VEVVSPKRGALSNHHVRLRRSTDMD 261

Query: 226 APAGLGE-PQLELHTLDLRDYGAQGDCDPEAPMTEGTR----------CCRQEMYIDLQG 274
             A     P L  +T D +                G +          C R  +Y+ L G
Sbjct: 262 DHAWQHRRPLLLTYTDDGKGSSNSNRVASRQKRANGRKKHQRRRLKANCRRHSLYVDFSD 321

Query: 275 MKWAKNWVLEPPGFLAYECVGTCQQP 300
           + W  +W++ PPG+ AY C G C  P
Sbjct: 322 VGW-NDWIVAPPGYQAYYCHGECPFP 346
```

sp O46576 BMP4_RABIT **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4] [Oryctolagus cuniculus (Rabbit)]** 409 AA align

```
 Score = 55.5 bits (132), Expect = 2e-06
 Identities = 58/224 (25%), Positives = 84/224 (36%), Gaps = 27/224 (12%)

Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE S    +F +   +P N  +  A LRLF+E V +        HR          A
Sbjct: 134 SENSAFRFLFNLSS-IPENEAISSAELRLFREQVDQGPDWERGFHRINIYEVMKPPAEAV 192

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQRE 206
                 G   T L+D+RLV  + + W+ FDV+ AV  W              V V
Sbjct: 193 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNHGLAVEVTHF 242

Query: 207 HLGPLASGAH-KLVRFASQGAPAGLGEPQLEL--------HTLDLRDYGAQG-DCDPEAP 256
           H      G H +L R   QG+        L +        H L  R    +    P+
Sbjct: 243 HHTRTHQGQHVRLSRSLLQGSGDWAQFRPLLVTFGHDGRGHALTRRRRAKRSLKHHPQRA 302

Query: 257 MTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
             +   C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 303 RKKNKNCRRHALYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 345
```

tr Q90Y82 **LjBmp2/4a (Fragment) [LjBmp2/4a] [Lampetra japonica (Japanese lamprey) (Entosphenus japonicus)]** 277 AA

align

Score = 55.1 bits (131), Expect = 2e-06
Identities = 59/229 (25%), Positives = 87/229 (37%), Gaps = 53/229 (23%)

```
Query: 107 LPPNSELVQAVLRLFQEPVP---KAALHR---HGRLSPRSAQARVTVEWLRVRDDGSNRT 160
           +P    +  A L +++E +    +AALHR   +  L P +A             DG+
Sbjct: 3   IPDGEVITSAELHVYRERLSGPARAALHRINVYEVLRPAAA-------------DGTPIA 49

Query: 161 SLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVR 220
            L+D+R+V    S W+ FDV+ A   W             + V+  HL        + VR
Sbjct: 50  RLLDTRVVHSGRSEWERFDVSPAAVRWAAARAPNHG----LLVEVHHLDGGTPEKRRHVR 105

Query: 221 F----------------ASQGAPAGLGEPQLEL------HTLDLRDYGAQGDCDPEA--- 255
                          A +G   G G PQL        H    RD G       P+
Sbjct: 106 IGRSLHAEAVAAAARDGAGEGGDGGEGWPQLRPLLVTFGHDGKTRDEGTLLRPRPKRNSR 165

Query: 256 PMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           P   G R    C R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 166 PNKGGRRGRGQCARYPLYVDFSDVGW-NDWIVAPPGYNAFFCQGECHFP 213
```

tr O96504 **Bone morphogenetic protein 2/4 [AmphiBMP2/4] [Branchiostoma floridae (Florida lancelet) (Amphioxus)]** 361 AA

align

Score = 55.1 bits (131), Expect = 2e-06
Identities = 53/205 (25%), Positives = 83/205 (39%), Gaps = 17/205 (8%)

```
Query: 109 PNSELVQAV-LRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRV--RDDGSNRTSLIDS 165
           P+ EL++A  LRLF+E +    + ++G  +          E +R   R +    T L+D+
Sbjct: 96  PSVELIKAAELRLFREQIDVDHV-QYGDSTDHHLYRVNVYEVMRPNSRTNTDTITRLLDT 154

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQG 225
           +LV V  S W++FDV  AV  W             V V     G L++   +L R
Sbjct: 155 KLVDVRNSSWESFDVRSAVTKWKNSPERNYGLE--VEVVSPKRGALSNHHVRLRRSTDMD 212

Query: 226 APAGLGE-PQLELHTLDLRDYGAQGDCDPEAPMTEGTR---------CCRQEMYIDLQGM 275
             +     P L  +T D +                G +         C R  +Y+D   +
Sbjct: 213 DHSWQHRRPLLLTYTDDGKGSSNSNRVASRQKRANGRKKQRRRLKANCRRHSLYVDFSDV 272

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
            W  +W++ PPG+ AY C G C  P
Sbjct: 273 GW-NDWIVAPPGYQAYYCHGECPFP 296
```

sp Q29607 BMP4_DAMDA **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4] [Dama dama (Fallow deer) (Cervus dama)]** 408 AA

align

Score = 54.3 bits (129), Expect = 3e-06
Identities = 56/227 (24%), Positives = 83/227 (35%), Gaps = 34/227 (14%)

```
Query: 92  SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
           SE S     +F +    +P N  +  A LR F+E V +         HR           A
Sbjct: 134 SENSAFRFLFNLS--IPENQVISTAELRDFREQVDQGPDWERGFHRINIYEVMKPPAEAV 191

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQRE 206
                    G    T L+D+RLV  + + W+ FDV+ AV  W              + V
Sbjct: 192 --------PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 241

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG--------AQGDCDP 253
           H       G H  +    S+  P G G+      P L     D R +                P
Sbjct: 242 HQTRTHQGQHVRI---SRSLPQGSGDWAQLRPLLVTFGHDGRGHALTRHRRAKRSPKHHP 298

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +    +   C R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 299 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344
```

tr Q9U5E8 **Pf-BMP2/4 [Pf-bmp2/4] [Ptychodera flava]** 405 AA
align

Score = 54.3 bits (129), Expect = 3e-06
Identities = 53/204 (25%), Positives = 86/204 (41%), Gaps = 14/204 (6%)

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAA--LHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTS-L 162
           +P N  +  A LRL+ + +  ++   +   R S      R+ V E L   D+G     L
Sbjct: 141 IPDNEVVTGAELRLYCQGINISSPMTNTDDRPSEYQFLHRINVHEILEPADEGGESIKRL 200

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVS-VQREHLGPLASGAHKLVRF 221
           IDS++V +  S W++FD+  AV  W              ++ VQ   + P     H  +R
Sbjct: 201 IDSKVVDIRNSSWESFDIRPAVAKWKASQEENHGVEVELTEVQNSQISPHKD--HVRLRR 258

Query: 222 ASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGMK 276
           +S  A A   + Q  L      D          +   +G R     C R+ +Y+D    +
Sbjct: 259 SSDLA-ASEWQRQRPLLITYTDDGKRPTRSKRNSERKKGGRKLKPNCRRRSLYVDFSDVG 317

Query: 277 WAKNWVLEPPGFLAYECVGTCQQP 300
           W  +W++ PPG+ A+ C G C  P
Sbjct: 318 W-NDWIVAPPGYNAFYCDGECPFP 340
```

sp O46564 BMP2_RABIT **Bone morphogenetic protein 2 precursor (BMP-2) [BMP2] [Oryctolagus cuniculus (Rabbit)]** 395 AA
align

Score = 53.9 bits (128), Expect = 4e-06
Identities = 51/216 (23%), Positives = 85/216 (38%), Gaps = 44/216 (20%)

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAA---------LHRHGRLSPRSAQARVTVEWLRVRDDGS 157
           +PP    +  A L++F+E + +A          ++ +   + P +A ++
Sbjct: 138 IPPEEFITSAELQVFREQMQEALGDDSGFHHRINIYEIIKPATANSKFPA---------- 187

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLG------PL 211
             T L+D+RLV+ + S W++FDVT AV  W              V+   E  G       +
Sbjct: 188 --TRLLDTRLVNQNTSRWESFDVTPAVMRWTAQGHANHGFVVEVTHLEEKQGVSKRHVRI 245
```

```
Query: 212 ASGAHKLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264
           +  H       SQ  P          G G P   LH  + R            +      + C
Sbjct: 246 SRSLHPDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR------QAKHKQRKRLKSSCK 296

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 297 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 331
```

sp O19006 BMP2_DAMDA **Bone morphogenetic protein 2 precursor (BMP-2) [BMP2] [Dama dama (Fallow deer) (Cervus dama)]** 396 AA align

```
 Score = 53.9 bits (128), Expect = 4e-06
 Identities = 52/216 (24%), Positives = 87/216 (40%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHR---HGRLS------PRSAQARVTVEWLRVRDDGS 157
           +P     +  A L++F + +P+A   +     H R++        P +A ++  V
Sbjct: 139 IPTEEFITSAELQVFGKHMPEALENNSSFHHRINIFEIIKPATANSKFPV---------- 188

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGP------L 211
              T L+D+RLV+ + S W++FDVT AV  W                V+    + G        +
Sbjct: 189 --TRLLDTRLVTQNASRWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSYGASKRHVRI 246

Query: 212 ASGAHKLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264
           +  H+      SQ  P          G G P   LH  + R            +      + C
Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR------QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           R  +Y+D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 332
```

tr Q9PVK1 **Anti-dorsalizing morphogenetic protein [ADMP] [Gallus gallus (Chicken)]** 364 AA align

```
 Score = 53.9 bits (128), Expect = 4e-06
 Identities = 57/208 (27%), Positives = 82/208 (39%), Gaps = 41/208 (19%)

Query: 123 EPVPKAALHRHGRLSPRSAQARVTVEWLRV---------RDDGSNRTSLIDSRLVSVHES 173
           E +  A LH    RL PR+A+          + +V               D          L+ +RL+S+  S
Sbjct: 102 EKILTAELHLF-RLWPRAAEGPRRHHFCQVSVYQILDESEPDSPEGQKLLATRLLSLQGS 160

Query: 174 GWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLGEP 233
           GW+ F +T+AV  W                V        LG  A  A    V+FAS G          +P
Sbjct: 161 GWEVFAITQAVRDWTQDESSNRGLLVTV----HGLGGSALEA-PAVQFASSGDHHESKKP 215

Query: 234 QLELHTLDLRDYGAQGDCDPEAPM-----------TEGTR----------CCRQEMYIDL 272
            L L T    D G +G    P A +                  G R                C R  + +D
Sbjct: 216 MLVLFT----DDGRRGASLPMAGVPASQPRDFPAKLSGPRSARSLDRLQPCQRHPLSVDF 271

Query: 273 QGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           + + W+   W++ P G+ AY C G+C  P
```

```
Sbjct: 272 EEIGWS-GWIISPRGYNAYHCRGSCPFP 298
```

sp P30884 BMPB_XENLA **Bone morphogenetic protein 2-II precursor (BMP-2-II) [Xenopus laevis (African clawed frog)]** 398 AA align

```
 Score = 53.1 bits (126), Expect = 8e-06
 Identities = 55/211 (26%), Positives = 89/211 (42%), Gaps = 37/211 (17%)

Query: 109 PNSELV-QAVLRLFQEPVPK------AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158
           P+ ELV  + LR+F+E V +      + LHR   +  + P +A +R  V
Sbjct: 142 PDEELVTSSELRIFREQVQEPFKTDGSKLHRINIYDIVKPAAAASRGPV---------- 190

Query: 159 RTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKL 218
              L+D+RL+  +ES W++FDVT A+  W              V+    HL    +   +
Sbjct: 191 -VRLLDTRLIHHNESKWESFDVTPAITRWIAHKQPNHGFVVEVT----HLDNDTNVPKRH 245

Query: 219 VRFASQGAPAGLGE-----PQLELHTLDLRDYGAQGDCDPEAPMTEGTR----CCRQEMY 269
           VR  S+      G      P L   + D + +         +A   +  R    C R  +Y
Sbjct: 246 VRI-SRSLTLDKGHWPRIRPLLVTFSHDGKGHALHKRQKRQARHKQRKRLKSSCRRHPLY 304

Query: 270 IDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +D   + W  +W++ PPG+ A+ C G C  P
Sbjct: 305 VDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 334
```

tr Q9VQG9 **CG16987-PA (Cg16987-pb) (GH14433p) [Alp23B] [Drosophila melanogaster (Fruit fly)]** 586 AA align

```
 Score = 53.1 bits (126), Expect = 8e-06
 Identities = 33/109 (30%), Positives = 53/109 (48%), Gaps = 20/109 (18%)

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ---QPPEALAFNWPFL------ 311
           T CCR+ +YI  + + W+ NW+L+P G+ AY C G+C        +A + +   +
Sbjct: 481 TECCREHLYISFRDIGWS-NWILKPEGYNAYFCRGSCSSVASVTQAASHHSSIMKILSTS 539

Query: 312 GPRQ-------CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
           G  +       C A + +SL ++V       T   V +LPNM V+ C C
Sbjct: 540 GANKSLELVPCCTAKQYSSLQLVVMDSSNTAT---VKTLPNMVVESCGC 585
```

sp O08717 IHBE_MOUSE **Inhibin beta E chain precursor (Activin beta-E chain) [Inhbe] [Mus musculus (Mouse)]** 350 AA align

```
 Score = 52.8 bits (125), Expect = 1e-05
 Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ-----QPPEALA 305
           C+PE P+     CCR++ Y+D Q + W ++W+L+P G+    C G C       P  A +
Sbjct: 240 CEPETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293
```

```
Query: 306 FN------------WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
           F+             WP  G   C+ +    L ++     G   +  V   P+M V+ C C
Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354
           +
Sbjct: 350 S 350
```

sp P12643 BMP2_HUMAN **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) [BMP2] [Homo sapiens (Human)]** 396 AA align

```
 Score = 52.8 bits (125), Expect = 1e-05
 Identities = 53/216 (24%), Positives = 86/216 (39%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHR---HGRLS------PRSAQARVTVEWLRVRDDGS 157
           +P    +  A L++F+E +  A  +    H R++      P +A ++  V
Sbjct: 139 IPTEEFITSAELQVFREQMQDALGNNSSFHHRINIYEIIKPATANSKFPV---------- 188

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLG------PL 211
             T L+D+RLV+ + S W++FDVT AV  W              V+   E  G       +
Sbjct: 189 --TRLLDTRLVNQNASRWESFDVTPAVMRWTAQGHANHGFVVEVAHLEEKQGVSKRHVRI 246

Query: 212 ASGAHKLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264
           +   H+     SQ  P        G G P   LH  + R          +      + C
Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHKREKR------QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           R  +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 332
```

tr Q91XH3 **Inhibin beta E [Inhbe] [Mus musculus (Mouse)]** 350 AA align

```
 Score = 52.8 bits (125), Expect = 1e-05
 Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ-----QPPEALA 305
           C+PE P+     CCR++ Y+D Q + W  ++W+L+P G+    C G C       P  A +
Sbjct: 240 CEPETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN------------WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
           F+             WP  G   C+ +    L ++     G   +  V   P+M V+ C C
Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354
           +
Sbjct: 350 S 350
```

tr Q7Q3Q7 **AgCP11289 (Fragment) [agCG50272] [Anopheles gambiae str. PEST]** 459 AA

align

```
 Score = 52.8 bits (125), Expect = 1e-05
 Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

Query: 41  PVLDRADMEKLVIPAHVRAQYVVLLRRS---------HGDRSRGKRFSQSFREVAGRFLA 91
           P   + D  K+VIP  ++  Y  ++              G  +R     +SF
Sbjct: 101 PNRPKIDRSKVVIPEAMKQLYAQIMGHDLVDSVSVPKEGLNTRNANTVRSFTHEESHIDQ 160

Query: 92  SEASTHL--LVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEW 149
                H   L+F +   +P   +L  A L L +E +     HR  R   R+       + +
Sbjct: 161 RFQHHHRFRLLFNVTS-IPRGEKLRAAELTLTREGIA----HRSSRAQARTPVLYQVMVY 215

Query: 150 LRVRDDGSNRTS----LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV---- 201
             VR     + +    L+D++ ++++ESG  +FDV  AV  W             V
Sbjct: 216 DIVRPGVKGKRAPTFLLVDTKTLAINESGTASFDVMPAVERWLRQPRKNHGLFVQVTGRG 275

Query: 202 ------SVQREHLGPLASGAHKLVRFASQGAPAGLG----EPQLELHTLD-------LRD 244
                 S QR  + P A   H+ VR     A          +P L  +T D       +RD
Sbjct: 276 RGPPGHSRQRRSIVP-AVPVHEHVRLRRNAAERHDSWVQKQPLLFTYTDDGRHKQRPIRD 334

Query: 245 YGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ 299
             +  +    A     +R     C R+ +Y+D   + W  +W++ PPG+ AY C G C+
Sbjct: 335 AISSANRARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGYEAYYCQGDCRF 393

Query: 300 P------------PEALAFNW-PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNM 346
           P             + L  ++ P L P+ C      S   ++ + E  + +  + +  +M
Sbjct: 394 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPTQLSSISMLYLNE--QNKVVLKNYQDM 451

Query: 347 RVQKCSC 353
            V  C C
Sbjct: 452 TVVGCGC 458
```

tr Q6PUC6 **Decapentaplegic (Fragment) [Anopheles gambiae (African malaria mosquito)]** 379 AA

align

```
 Score = 52.8 bits (125), Expect = 1e-05
 Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

Query: 41  PVLDRADMEKLVIPAHVRAQYVVLLRRS---------HGDRSRGKRFSQSFREVAGRFLA 91
           P   + D  K+VIP  ++  Y  ++              G  +R     +SF
Sbjct: 21  PNRPKIDRSKVVIPEAMKQLYAQIMGHDLVDSVSVPKEGLNTRNANTVRSFTHEESHIDQ 80

Query: 92  SEASTHL--LVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEW 149
                H   L+F +   +P   +L  A L L +E +     HR  R   R+       + +
Sbjct: 81  RFQHHHRFRLLFNVTS-IPRGEKLRAAELTLTREGIA----HRSSRAQARTPVLYQVMVY 135

Query: 150 LRVRDDGSNRTS----LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV---- 201
             VR     + +    L+D++ ++++ESG  +FDV  AV  W             V
Sbjct: 136 DIVRPGVKGKRAPTFLLVDTKTLAINESGTASFDVMPAVERWLRQPRKNHGLFVQVTGRG 195

Query: 202 ------SVQREHLGPLASGAHKLVRFASQGAPAGLG----EPQLELHTLD-------LRD 244
                 S QR  + P A   H+ VR     A          +P L  +T D       +RD
```

```
Sbjct: 196 RGPPGHSRQRRSIVP-AVPVHEHVRLRRNAAERHDSWVQKQPLLFTYTDDGRHKQRPIRD 254

Query: 245 YGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ 299
             +  +    A     +R     C R+ +Y+D   + W  +W++ PPG+ AY C G C+
Sbjct: 255 AISSANRARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGYEAYYCQGDCRF 313

Query: 300 P------------PEALAFNW-PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNM 346
            P             + L  ++ P L P+ C      S   ++ + E  + +  + +  +M
Sbjct: 314 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPTQLSSISMLYLNE--QNKVVLKNYQDM 371

Query: 347 RVQKCSC 353
            V  C C
Sbjct: 372 TVVGCGC 378
```

tr Q9W6T9 **Activin beta B protein (Fragment) [inhbb] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 138 AA

align

```
 Score = 52.0 bits (123), Expect = 2e-05
 Identities = 37/140 (26%), Positives = 62/140 (43%), Gaps = 25/140 (17%)

Query: 231 GEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLA 290
           G  QL+L  L +   G+  +CD        G  CCRQ+ YID + + W  +W++ P G+
Sbjct: 1   GLEQLKLACLQVDSRGSGFECDGN----NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYG 55

Query: 291 YECVGTCQQ-----PPEALAFNWPFLGPRQ------------CIASETASLPMIVSIKEG 333
             C G+C        P  A +F+   +  +            CI  ++ +++ M+    E
Sbjct: 56  NYCEGSCPAYMAGVPGSASSFHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEY 115

Query: 334 GRTRPQVVSLPNMRVQKCSC 353
             +  V   PNM V++C C
Sbjct: 116 NIVKRDV---PNMIVEECGC 132
```

tr Q9PWR8 **Activin beta B subunit precursor [Carassius auratus (Goldfish)]** 392 AA

align

```
 Score = 52.0 bits (123), Expect = 2e-05
 Identities = 79/353 (22%), Positives = 131/353 (36%), Gaps = 66/353 (18%)

Query: 42  VLDRADMEKLVIPAHV--RAQYVVLLRRSHGDRSR--GKRFSQSFREVAGRFLASEASTH 97
           +L+R  M +     H   +A  V  LR+ H  + R  G+    +F   A      E ++
Sbjct: 66  ILNRLQMRERPNITHPIPKAAMVTALRKLHAGKVREDGRVEIPNFDGHAAHNEVQEETSE 125

Query: 98  LLVFGMEQRLPPNSELVQAVLRLFQEP---VPKAALHRHGRLSP----RSAQARVTVEWL 150
           ++ F     + P+   +  ++          V +A L  + +L P    +  + +VTV
Sbjct: 126 IISFAESDDVTPSKSSLYFLISNEGNQNLYVLQANLWLYFKLLPGTQEKGLRRKVTVRVR 185

Query: 151 RVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGP 210
               G N    +  + V +  SGW   F V+EAV                  RE L
Sbjct: 186 SYEPGGQNVHWPMMEKRVELKRSGWHTFPVSEAV--------------------REMLAK 225

Query: 211 LASGAHKLVRFASQGAPAG-----LGEPQLELHTLDLRDYGAQGDCDP-------EAPMT 258
```

```
              G  + +    +G  A      L +P    H   L     Q D          E   T
Sbjct: 226 --GGRRQDLDIHCEGCEAANVLPILVDPSDPSHRPFLVVRAQQADSKHRIRKRGLECDGT 283

Query: 259 EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ-----PPEALAFNWPFLGP 313
            G  CCRQ+ YID + + W  +W++ P G+    C G+C       P  A +F+   +
Sbjct: 284 NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQ 342

Query: 314 RQ------------CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA 354
            +             CI ++ +++ M+    E    +  V   PNM V++C CA
Sbjct: 343 YRMRGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGCA 392
```

tr Q869H8 **GDF2 precursor [Crassostrea gigas (Pacific oyster)]** 387 AA

align

Score = 52.0 bits (123), Expect = 2e-05
Identities = 49/217 (22%), Positives = 85/217 (38%), Gaps = 31/217 (14%)

```
Query: 161 SLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVR 220
           +L++SR + +   GW+ FD+T+ V  W              + V     G L   +  +
Sbjct: 179 TLVESRTIDLSRDGWEIFDITQDVQDWIEDPELNNGIE--IFVDGLDAGQLVFPSLNITE 236

Query: 221 FASQGAPAGLGEPQLELHTLDLRDYGA--------QGDCDP-EAPMTEG-TRCCRQEMYI 270
             S  +      P + L  L+++ +          Q D +  +    +G +RCCR    I
Sbjct: 237 RMSSKSSTNTTIPNVILPILEMKTHERSILKRVKRQNDIERRDCVKGDGESRCCRFTTTI 296

Query: 271 DLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLG-------------PRQCI 317
              + W  +W+L PP + A+ C G+C    P+       F G              P+ C
Sbjct: 297 AFSDLGW-NDWILAPPDYEAHYCDGSC---PDRFKMANTFAGIQARLHALYPNKFPKPCC 352

Query: 318 ASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA 354
               S P+ +  K+    + Q+   P+M V+ C CA
Sbjct: 353 VPSKLS-PLTILHKDSS-GKYQLTDYPDMIVEDCKCA 387
```

tr Q8MKC2 **Bone morphogenetic protein 2 (Fragment) [Ovis aries (Sheep)]** 223 AA

align

Score = 51.6 bits (122), Expect = 2e-05
Identities = 41/154 (26%), Positives = 63/154 (40%), Gaps = 23/154 (14%)

```
Query: 160 TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGP------LAS 213
           T L+D+RLV+ + S W++FDVT AV  W              V+   +  G        ++
Sbjct: 42  TRLLDTRLVTQNASRWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSHGASKRHVRISR 101

Query: 214 GAHKLVRFASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQ 266
             H+      SQ  P         G G P    LH  + R           +       + C R
Sbjct: 102 SLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR------QAKHKQRKRLKSSCKRH 152

Query: 267 EMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
            +Y+D    + W  +W++ PPG+ A+ C G C  P
Sbjct: 153 PLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPFP 185
```

tr Q8IAE3 **Sj-BMP2/4 [Sj-bmp2/4] [Stichopus japonicus (Sea cucumber)]** 422 AA

align

Score = 51.2 bits (121), Expect = 3e-05
Identities = 62/250 (24%), Positives = 94/250 (36%), Gaps = 30/250 (12%)

```
Query: 80  QSFREVAGRFLASEA-STHLLVFGMEQRLPPNSELVQAVLRLFQEPVP------KAALHR 132
           +SF  +   F   EA   H LVF +   +     L  A LRLF+  +P      + AL+
Sbjct: 118 KSFHHIEEHFDIDEAIHRHRLVFNLSS-IENEEILTAAELRLFRHAIPDHKIRKRHALNE 176

Query: 133 HGRLSPRSAQARVTVEWLRVRDDGSNRT---SLIDSRLVSVHESGWKAFDVTEAVNFWXX 189
              ++      R+ +  + ++    NR     LIDS ++ V  + W++ DV  AV  W
Sbjct: 177 SENITDGKVIQRINLYQI-LKPVARNRDVIKRLIDSIVIDVRNTTWESLDVAPAVKSWTN 235

Query: 190 XXXXXXXXXXXVSVQREHLGPLASGAHKLVRFASQGAPAGLG----------EPQLELHT 239
                    +  +R    P   G   L      G  A L             P L  +T
Sbjct: 236 DANSNYGVEIEIIDRRG--SPSRHGDDHLRTRRRIGDDASLEIHDEDQWFQQRPLLVTYT 293

Query: 240 LDLRDYGAQGDCDPEAPMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVG 295
            D R   +           +  R    C +  +Y+D   + W  +W+L P G+ AY C G
Sbjct: 294 DDGRTKRSSKKRTKRQKSKKKRRLKENCSKHSLYVDFAIVGW-DSWILAPEGYQAYYCQG 352

Query: 296 TCQQP-PEAL 304
           C  P PE L
Sbjct: 353 ECPYPMPEHL 362
```

tr Q6XDQ0 **Bone morphogenetic protein 2 [Gallus gallus (Chicken)]** 392 AA
align

Score = 50.4 bits (119), Expect = 5e-05
Identities = 57/213 (26%), Positives = 86/213 (39%), Gaps = 41/213 (19%)

```
Query: 109 PNSELV-QAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNR---TSLID 164
           PN E V  A L++F+E V +A        S  S   R+ +  +      +++   T L+D
Sbjct: 136 PNEESVTSAELQIFREQVHEAFE------SNSSYHHRINIYEIMKPATATSKDPVTRLLD 189

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQREHLGPLASGAHKLVRFA-- 222
           +RLV  + S W++FDVT AV  W                V+  HL    S + + VR +
Sbjct: 190 TRLVHHNASKWESFDVTPAVLRWIAHGQPNHGFV----VEVVHLDKENSASKRHVRISRS 245

Query: 223 --------SQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQE 267
                  SQ  P        G G P   LH  + R          +        C R
Sbjct: 246 LHQDEDSWSQLRPLLVTFGHDGKGHP---LHKREKRQ------AKHKQRKRHKYSCKRHP 296

Query: 268 MYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           +Y+D   + W  +W++ PPG+ A+  C G C  P
Sbjct: 297 LYVDFNDVGW-NDWIVAPPGYSAFYCHGECPFP 328
```

sp P27093 IHBB_CHICK **Inhibin beta B chain precursor (Activin beta-B chain) [INHBB] [Gallus gallus (Chicken)]** 391 AA
align

Score = 50.1 bits (118), Expect = 6e-05

tr O13109 **BMP2 [bmp2a] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 386 AA

align

Score = 50.1 bits (118), Expect = 6e-05
Identities = 68/252 (26%), Positives = 102/252 (39%), Gaps = 47/252 (18%)

```
Query: 65  LRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELV-QAVLRLFQE 123
           +R  H D S     S S R    RFL +  S             P+ ELV  A +R+F+E
Sbjct: 102 IRSFHHDESTEDPSSSSVRTTQ-RFLFNLTSI----------PDEELVTSADVRVFRE 148

Query: 124 PVPKAALHRHGRLSPRSAQA-RVTVEWLRVRDDGSNR---TSLIDSRLVSVHESGWKAFD 179
            +  +       L+  SA   R+ V  + +R  GS +   T L+D+RLV    S W++FD
Sbjct: 149 QIVSS-------LNNASAGFHRINVHEI-IRPSGSLQEPITRLLDTRLVQHSLSKWESFD 200

Query: 180 VTEAVNFWXXXXXXXXXXXXXVSV----QREHLGPLASGAHKLVRFASQGAPA------- 228
           VT AV  W              +S      R+H+  ++   H      SQ  P
Sbjct: 201 VTPAVLKWTTDGHPNHGILVEISHPDQDSRKHVR-VSRSLHNNEDTWSQMRPLLVTYSHD 259

Query: 229 GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGF 288
           G G     LH+ + R        + +        C R  +Y+D   + W  +W++ PPG+
Sbjct: 260 GKGNV---LHSREKRQAR-----NNKQRKKHKANCRRHSLYVDFSDVGW-NDWIVAPPGY 310

Query: 289 LAYECVGTCQQP 300
            A+ C G C  P
Sbjct: 311 HAFYCQGECPFP 322
```

sp O88959 IHBE_RAT **Inhibin beta E chain precursor (Activin beta-E chain) [Inhbe] [Rattus norvegicus (Rat)]** 350 AA align

Score = 49.7 bits (117), Expect = 8e-05
Identities = 32/121 (26%), Positives = 53/121 (43%), Gaps = 27/121 (22%)

```
Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ-----QPPEALA 305
           C+ E P+     CCR++ Y+D Q + W ++W+L+P G+    C G C        P  A +
Sbjct: 240 CESETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN----------WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
           F+           WP  G   C+ +    L ++     G   +  V   P+M V+ C C
Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354
           +
Sbjct: 350 S 350
```

sp P17491 IHBB_RAT **Inhibin beta B chain precursor (Activin beta-B chain) [Inhbb] [Rattus norvegicus (Rat)]** 411 AA align

Score = 49.7 bits (117), Expect = 8e-05

```
 Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

Query: 81  SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRS 140
           SF E  G   LAS   S    L F +       N  +VQA L L+ + +P            +
Sbjct: 149 SFAETDG--LAS--SRVRLYFFVSNEGNQNLFVVQASLWLYLKLLPYVL--------EKG 196

Query: 141 AQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXX 200
           ++ +V V+          +R ++++ + V +  SGW   F +TEA+
Sbjct: 197 SRRKVRVKVYFQEQGHGDRWNVVEKK-VDLKRSGWHTFPITEAIQ----ALFERGERRLN 251

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEG 260
           + VQ +    LA     +         P  + + +L       +R  G +  CD    +
Sbjct: 252 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLE--CDGRTSL--- 306

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ-----PPEALAFNWPFL---- 311
             CCRQ+ +ID + + W  +W++ P G+    C G+C        P  A +F+   +
Sbjct: 307 --CCRQQFFIDFRLIGW-NDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 363

Query: 312 ------GPRQ--CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA 354
                 GP    CI ++ +S+ M+    E    +  V   PNM V++C CA
Sbjct: 364 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV---PNMIVEECGCA 411
```

sp Q04999 IHBB_MOUSE **Inhibin beta B chain precursor (Activin beta-B chain) (Fragment) [Inhbb] [Mus musculus (Mouse)]** 367 AA align

```
 Score = 49.7 bits (117), Expect = 8e-05
 Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

Query: 81  SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRS 140
           SF E  G   LAS   S    L F +       N  +VQA L L+ + +P            +
Sbjct: 105 SFAETDG--LAS--SRVRLYFFVSNEGNQNLFVVQASLWLYLKLLPYVL--------EKG 152

Query: 141 AQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXX 200
           ++ +V V+          +R ++++ + V +  SGW   F +TEA+
Sbjct: 153 SRRKVRVKVYFQEQGHGDRWNVVEKK-VDLKRSGWHTFPITEAIQ----ALFERGERRLN 207

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEG 260
           + VQ +    LA     +         P  + + +L       +R  G +  CD    +
Sbjct: 208 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLE--CDGRTSL--- 262

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ-----PPEALAFNWPFL---- 311
             CCRQ+ +ID + + W  +W++ P G+    C G+C        P  A +F+   +
Sbjct: 263 --CCRQQFFIDFRLIGW-NDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 319

Query: 312 ------GPRQ--CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA 354
                 GP    CI ++ +S+ M+    E    +  V   PNM V++C CA
Sbjct: 320 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV---PNMIVEECGCA 367
```

sp O95393 BM10_HUMAN **Bone morphogenetic protein 10 precursor (BMP-10) [BMP10] [Homo sapiens (Human)]** 424 AA align

```
 Score = 49.7 bits (117), Expect = 8e-05
 Identities = 50/235 (21%), Positives = 88/235 (37%), Gaps = 50/235 (21%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGS---NRTSL 162
           +P + E++ A LRL+        L +  R+       ++T+ E L  + D     N   L
Sbjct: 134 IPHHEEVIMAELRLY-------TLVQRDRMIYDGVDRKITIFEVLESKGDNEGERNMLVL 186

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHK----- 217
           +   +   + S W+ FDVT+A+  W             +  + +     +SG  +
Sbjct: 187 VSGEIYGTN-SEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLEIDTSA 245

Query: 218 -------LVRFASQGAPAGLGEPQL----------ELHTLDLRDYGAQGDCDPEAPM--- 257
                 L+ F+   +     + +L          EL  L L  + +    +    M
Sbjct: 246 QNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGEEALLQMRSN 305

Query: 258 ------------TEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                      +G  C R  +YID + + W  +W++ PPG+ AYEC G C  P
Sbjct: 306 IIYDSTARIRRNAKGNYCKRTPLYIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 359
```

sp P48969 DVR1_STRPU **DVR-1 protein homolog precursor [DVR1] [Strongylocentrotus purpuratus (Purple sea urchin)]** 461 AA

align

```
 Score = 49.3 bits (116), Expect = 1e-04
 Identities = 50/226 (22%), Positives = 88/226 (38%), Gaps = 49/226 (21%)

Query: 106 RLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVR-DDGSNRTSLID 164
           R+P    +  A LR+F++        R GR     +  R+ V  LR R  DGS     +D
Sbjct: 189 RIPQGETVTSAELRVFRDA------GRQGR-----SLYRIDVLLLRERGSDGSRSPVYLD 237

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV-SVQREHLGP------------- 210
           S +V   + GW  FD+T A + W              V S+Q  ++ P
Sbjct: 238 STIVGAGDHGWLVFDMTSATSTWRSYPGANVGLQLRVESLQGLNIDPTDAGVVGVGNNEG 297

Query: 211 ---------------LASGAH-KLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPE 254
                         +A+ +H +  R A+     G   P+      D+          D
Sbjct: 298 REPFMVVFFQRNEEVIATNSHLRRNRRAATRQKKGGKRPRKPDTDNDI------ASRDSA 351

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
           + +    +C R+ ++++ + + W + W++ P G++A+ C G C  P
Sbjct: 352 SSLNSDWQCKRKNLFVNFEDLDW-QEWIIAPLGYVAFYCQGECAFP 396
```

tr Q90261 **Activin beta B [inhbb] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 393 AA

align

```
 Score = 49.3 bits (116), Expect = 1e-04
 Identities = 59/249 (23%), Positives = 94/249 (37%), Gaps = 63/249 (25%)

Query: 139 RSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXX 198
           +  +A+VTV        G N    +  + V +  SGW  F V+EA+
Sbjct: 175 KGLRAKVTVRVHSYEPGGQNVHWPMMEKRVELKRSGWHTFPVSEAI------------- 220
```

```
Query: 199 XXVSVQREHLGPLASGAHKLVRFASQGAPAG-----LGEPQLELHT--LDLRDYGAQG-- 249
           RE L     G  + +    +G  A      L +P    H   L +R   A G
Sbjct: 221 ------REMLAK--GGRRQDLDIHCEGCEAANVLPILVDPSDPSHRPFLVVRAQQADGKH 272

Query: 250 -------DCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ--- 299
                +CD       G  CCRQ+ YID + + W  +W++ P G+    C G+C
Sbjct: 273 RIRKRGLECDGN----NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMA 327

Query: 300 --PPEALAFNWPFLGPRQ------------CIASETASLPMIVSIKEGGRTRPQVVSLPN 345
             P  A +F+    +   +             CI ++ +++ M+    E    +  V   PN
Sbjct: 328 GVPGSASSFHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PN 384

Query: 346 MRVQKCSCA 354
           M V++C CA
Sbjct: 385 MIVEECGCA 393
```

tr Q869H7 **GDF3 precursor (Fragment) [Crassostrea gigas (Pacific oyster)]** 251 AA

align

```
 Score = 49.3 bits (116), Expect = 1e-04
 Identities = 56/238 (23%), Positives = 95/238 (39%), Gaps = 57/238 (23%)

Query: 162 LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV-----SVQREHLGPLASGAH 216
           +ID++ V   +SGW+ FDVT AV  W             +     SV    L  L    H
Sbjct: 24  VIDTQHVYGRDSGWETFDVTSAVRRWVTKPSSSQILEIRIESVFHSVTDGDLDFLTEPQH 83

Query: 217 K----LVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDC--DPEAPMT------------ 258
           K    LV F++         + +L+LH  +  +   + D   D ++P++
Sbjct: 84  KNEPLLVVFSTD-------KQKLQLHKTERHELITREDSIYDIQSPLSGSKNSNNSLNET 136

Query: 259 -----------------EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPP 301
                           G  C R+ M ++   ++W  +W+L P  + AYECVG C  P
Sbjct: 137 NTIGHKIHSRVKRRGRRSGGLCRRRPMTVNFADIQW-DSWILAPSSYEAYECVGKCHFPV 195

Query: 302 E---ALAFNWPFLGPRQ--CIASETASLPMIVSIKEGGRT-RPQVVSLPNMRVQKCSC 353
              + +   P   PR+  C+ ++  S+ ++   + G  T +P+      M V +C C
Sbjct: 196 NERLSPSLTMPKEYPRESCCVPTKLDSISILYYDEYGVLTYKPK---YDGMVVTECGC 250
```

sp P09529 IHBB_HUMAN **Inhibin beta B chain precursor (Activin beta-B chain) [INHBB] [Homo sapiens (Human)]** 407 AA

align

```
 Score = 48.5 bits (114), Expect = 2e-04
 Identities = 67/291 (23%), Positives = 116/291 (39%), Gaps = 45/291 (15%)

Query: 81  SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRS 140
           SF E  G  LAS  S   L F +      N  +VQA L L+ + +P            +
Sbjct: 145 SFAETDG--LAS--SRVRLYFFISNEGNQNLFVVQASLWLYLKLLPYVL--------EKG 192

Query: 141 AQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXX 200
           ++ +V V+         +R ++++ R V +  SGW   F +TEA+
Sbjct: 193 SRRKVRVKVYFQEQGHGDRWNMVEKR-VDLKRSGWHTFPLTEAIQ----ALFERGERRLN 247
```

```
Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEG 260
           + VQ +    LA     +         P  + + +L       +R  G +  CD    +
Sbjct: 248 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLE--CDGRTNL--- 302

Query: 261 TRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ-----PPEALAFNWPFLGPRQ 315
             CCRQ+ +ID + + W  +W++ P G+    C G+C       P  A +F+   +   +
Sbjct: 303 --CCRQQFFIDFRLIGW-NDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 359

Query: 316 ------------CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCA 354
                     CI ++ +++ M+    E    +  V   PNM V++C CA
Sbjct: 360 MRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGCA 407
```

tr Q9PTF9 **Bone morphogenetic protein 7 [bmp7] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 432 AA align

```
 Score = 48.5 bits (114), Expect = 2e-04
 Identities = 46/173 (26%), Positives = 66/173 (37%), Gaps = 44/173 (25%)

Query: 162 LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXVSVQR---------------- 205
           L+DSR+V   E GW  FD+T   N W              V
Sbjct: 205 LLDSRVVWAAEEGWLVFDLTVTSNHWVINPGQNLGLQLLVETSHGARMNPRRAGLVGSSG 264

Query: 206 -EHLGPL------ASGAH-KLVRFASQG----------APAGLGEPQLELHTLDLRDYGA 247
            ++  P       ASG H + VR AS G          A  G    Q+ L T +  + GA
Sbjct: 265 AQNKQPFMVAFLKASGIHLRSVRSASGGKQKGHHRTKNAKPGAAHSQVALKTAEATE-GA 323

Query: 248 QGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
               DP+         C + E+Y+  + + W ++W++ P G+ AY C G C  P
Sbjct: 324 S--IDPKQG------CKKHELYVSFRDLGW-QDWIIAPEGYAAYYCEGECVFP 367
```

tr Q6EH35 **Bone morphogenetic protein 2 (Fragment) [BMP-2] [Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta)]** 285 AA align

```
 Score = 48.5 bits (114), Expect = 2e-04
 Identities = 51/207 (24%), Positives = 83/207 (39%), Gaps = 29/207 (14%)

Query: 109 PNSE-LVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRL 167
           PN E L  A L++F+E V +   +         +    +        +D  +    L+D+RL
Sbjct: 33  PNEEFLTSAELQIFREQVQETFENNSSYHHRINIYEIIEAATATSKDPAAR---LLDTRL 89

Query: 168 VSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXV-------SVQREHLGPLASGAHKLVR 220
           V  + S W++FDVT AV  W              V        SV + H+  ++    H+
Sbjct: 90  VHQNASKWESFDVTPAVMRWIAHRQPNHGFIVEVVHLDNESSVSKRHVR-ISRSLHQDED 148

Query: 221 FASQGAPA-------GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQ 273
             SQ  P         G G       H+L  R+   +      +       + C R  +Y+D
Sbjct: 149 SWSQLRPLLVTFGHDGKG------HSLHKRE---KRQAKHKQRKRHKSSCKRHPLYVDFN 199

Query: 274 GMKWAKNWVLEPPGFLAYECVGTCQQP 300
            + W  +W++ PPG+ A+ C G C  P
```

```
Sbjct: 200 DVGW-NDWIVAPPGYGAFYCHGECPFP 225
```

sp P58166 IHBE_HUMAN **Inhibin beta E chain precursor (Activin beta-E chain) [INHBE] [Homo sapiens (Human)]** 350 AA align

```
 Score = 48.1 bits (113), Expect = 2e-04
 Identities = 31/121 (25%), Positives = 52/121 (42%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ-----QPPEALA 305
           C+P  P+     CCR++ Y+D Q + W ++W+L+P G+    C G C       P  A +
Sbjct: 240 CEPATPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN------------WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
           F+             WP      C+ +    L ++     G   +  V   P+M V+ C C
Sbjct: 294 FHSAVFSLLKANNPWP-ASTSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354
           +
Sbjct: 350 S 350
```

sp Q9R229 BM10_MOUSE **Bone morphogenetic protein 10 precursor (BMP-10) [Bmp10] [Mus musculus (Mouse)]** 420 AA align

```
 Score = 48.1 bits (113), Expect = 2e-04
 Identities = 57/234 (24%), Positives = 89/234 (37%), Gaps = 51/234 (21%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSN--RTSLID 164
           +P + E+V A LRL+        L +  R+       ++T+  +    DGS   R+ L+
Sbjct: 133 IPHHEEVVMAELRLY-------TLVQRDRMMYDGVDRKITIFEVLESADGSEEERSMLV- 184

Query: 165 SRLVSVH----ESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSVQREHLGPLASGAHK--- 217
             LVS       S W+ FDVT+A   W              +  ++         G  +
Sbjct: 185 --LVSTEIYGTNSEWETFDVTDATRRWQKSGPSTHQLEIHIESRQNQAEDTGRGQLEIDM 242

Query: 218 ---------LVRFASQGAPAGLGEPQL-ELHT----LDLRDYGAQGDCDPEAPM------ 257
                  LV F+    +     + +L EL T    LDL          D EA +
Sbjct: 243 SAQNKHDPLLVVFSDDQSNDKEQKEELNELITHEQDLDLDSDAFFSGPDEEALLQMRSNM 302

Query: 258 -----------TEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
                     +G  C +  +YID + + W  +W++ PPG+ AYEC G C  P
Sbjct: 303 IDDSSTRIRRNAKGNYCKKTPLYIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 355
```

sp Q24735 60A_DROVI **60A protein precursor (Glass bottom boat protein) [gbb] [Drosophila virilis (Fruit fly)]** 436 AA align

```
 Score = 48.1 bits (113), Expect = 2e-04
 Identities = 60/283 (21%), Positives = 103/283 (36%), Gaps = 47/283 (16%)
```

```
Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSR 166
           +P ++ L+ A LR++Q           G+ +  + Q  VTV  LR       N    + S
Sbjct: 164 IPTDNYLMMAELRIYQNS-------NEGKWTTTNKQFTVTVYMLRSGGSAPNMLEPLSSV 216

Query: 167 LVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSV----QREHLGPLASGAHKLVRFA 222
             +    GW   +VTEA++ W                      +RE         H+  +
Sbjct: 217 NTTGDYVGWLELNVTEALHDWRVNSNENHGIYIGAHALNKPEREIKLDDIGLIHRRTKVD 276

Query: 223 SQGAPAGLG----------------EPQLELHTLDLRDYGAQGDCDPEAPMT-EGTRCCR 265
            +  P  +G                + + +  TL  R        +P    + E TR C+
Sbjct: 277 DENQPFMIGFFRGPELIKSTSGHSTQKRTKRSTLHQRKKSKSEPVNPFIENSIENTRSCQ 336

Query: 266 -QEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEA-------------LAFNWPFL 311
            Q +YID + + W  +W++ P G+ A+ C G C  P  A             +    P
Sbjct: 337 MQTLYIDFKDLGW-HDWIIAPEGYGAFYCSGECNFPLNAHMNATNHAIVQTLVHLLEPKR 395

Query: 312 GPRQCIA-SETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
            P+ C A +   +LP++  + +       +    NM V+ C C
Sbjct: 396 VPKPCCAPTRLGALPVLYHLND---ENVNLKKYRNMIVKSCGC 435
```

tr Q9DGF1 **Inhibin/activin (Fragment) [Cyprinus carpio (Common carp)]** 115 AA

align

Score = 48.1 bits (113), Expect = 2e-04
Identities = 31/117 (26%), Positives = 52/117 (43%), Gaps = 21/117 (17%)

```
Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ-----PPEALAFNW 308
           E   T G  CCRQ+ YID + + W  +W++ P G+    C G+C       P  A +F+
Sbjct: 3   ECDGTNGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHT 61

Query: 309 PFLGPRQ----------CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
             +   +           CI ++ +++ M+    E    +  V   PNM V++C C
Sbjct: 62  AVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGC 115
```

```
Database: EXPASY/UniProt
    Posted date:  Nov 8, 2004  3:52 PM
  Number of letters in database: 518,174,383
  Number of sequences in database:  1,621,919

Lambda     K      H
   0.322    0.136    0.436

Gapped
Lambda     K      H
   0.267   0.0410    0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
length of query: 366
length of database: 518,174,383
effective HSP length: 126
```

```
effective length of query: 240
effective length of database: 313,812,589
effective search space: 75315021360
effective search space used: 75315021360
T: 11
A: 40
X1: 16 ( 7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 74 (33.1 bits)
```

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CLUSTAL W (1.74) multiple sequence alignment

```
sp|O00292|TGF4_HUMAN      MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIPAHVRA
sp|O75610|LFTB_HUMAN      MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRA
tr|Q8BMF7                 MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIPTHVRS
sp|P57785|LFTB_MOUSE      MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIPTHVRS
sp|Q64280|TGF4_MOUSE      MPFLWLCWALWALSLVSLREALTGEQILGSLLQQLQLDQPPVLDKADVEGMVIPSHVRT
                          *  ********.*.*..   *:* **:*.***:****.: *.** **:* :.**:***:

sp|O00292|TGF4_HUMAN      YVVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLR
sp|O75610|LFTB_HUMAN      YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLR
tr|Q8BMF7                 YVALLQGSHADRSRGKRFSQNFREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLR
sp|P57785|LFTB_MOUSE      YVALLQGSHADRSRGKRFSQNLREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLR
sp|Q64280|TGF4_MOUSE      YVALLQHSHASRSRGKRFSQNLREVAGRFLVSETSTHLLVFGMEQRLPPNSELVQAVLR
                          **.**: **..*********.:********  *:*************************

sp|O00292|TGF4_HUMAN      FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFD
sp|O75610|LFTB_HUMAN      FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFD
tr|Q8BMF7                 FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRTALIDSRLVSIHESGWKAFD
sp|P57785|LFTB_MOUSE      FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRTALIDSRLVSIHESGWKAFD
sp|Q64280|TGF4_MOUSE      FQEPVPRTALRRQKRLSPHSARARVTIEWLRFRDDGSNRTALIDSRLVSIHESGWKAFD
                          ******::**:*  ****:**:****:****.*:******:********:*********

sp|O00292|TGF4_HUMAN      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLEL
sp|O75610|LFTB_HUMAN      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLEL
tr|Q8BMF7                 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGEPQLEL
sp|P57785|LFTB_MOUSE      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGEPQLEL
sp|Q64280|TGF4_MOUSE      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQGTPDGKGQGEPQLEL
                          ****************************** : .:*******:**:*   * *******

sp|O00292|TGF4_HUMAN      TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTC
sp|O75610|LFTB_HUMAN      TLDLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTC
tr|Q8BMF7                 TLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSC
sp|P57785|LFTB_MOUSE      TLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSC
sp|Q64280|TGF4_MOUSE      TLDLKDYGAQGNCDPEAPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSC
                          **** ******:****.*:************:********:**:*******:*****:*

sp|O00292|TGF4_HUMAN      QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDG
sp|O75610|LFTB_HUMAN      QPPEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDG
tr|Q8BMF7                 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDG
sp|P57785|LFTB_MOUSE      QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDG
sp|Q64280|TGF4_MOUSE      QLPESLTSRWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDG
                          * **:*:  *********:***  *******:*******************.*******

sp|O00292|TGF4_HUMAN      LVPRRLQP
sp|O75610|LFTB_HUMAN      LVPRRLQP
tr|Q8BMF7                 LIPRGIDL
sp|P57785|LFTB_MOUSE      LIPRGIDL
sp|Q64280|TGF4_MOUSE      LIPRRLQP
                          *:** ::
```

PileUp

MSF: 368 Type: P Check: 4364 ..

Name: sp|O00292|TGF4_HUMAN oo Len: 368 Check: 6379 Weight: 0.100
Name: sp|O75610|LFTB_HUMAN oo Len: 368 Check: 6179 Weight: 0.100
Name: tr|Q8BMF7 oo Len: 368 Check: 9710 Weight: 0.100
Name: sp|P57785|LFTB_MOUSE oo Len: 368 Check: 9860 Weight: 0.100
Name: sp|Q64280|TGF4_MOUSE oo Len: 368 Check: 2236 Weight: 0.100

//

```
sp|O00292|TGF4_HUMAN      MWPLWLCWAL WVLPLAGPGA ALTEEQLLGS LLRQLQLSEV PVLDRADMEK
sp|O75610|LFTB_HUMAN      MQPLWLCWAL WVLPLASPGA ALTGEQLLGS LLRQLQLKEV PTLDRADMEE
tr|Q8BMF7                 MKSLWLCWAL WVLPLAGPGA AMTEEQVLSS LLQQLQLSQA PTLDSADVEE
sp|P57785|LFTB_MOUSE      MKSLWLCWAL WVLPLAGPGA AMTEEQVLSS LLQQLQLSQA PTLDSADVEE
sp|Q64280|TGF4_MOUSE      MPFLWLCWAL WALSLVSLRE ALTGEQILGS LLQQLQLDQP PVLDKADVEG

sp|O00292|TGF4_HUMAN      LVIPAHVRAQ YVVLLRRSHG DRSRGKRFSQ SFREVAGRFL ASEASTHLLV
sp|O75610|LFTB_HUMAN      LVIPTHVRAQ YVALLQRSHG DRSRGKRFSQ SFREVAGRFL ALEASTHLLV
tr|Q8BMF7                 MAIPTHVRSQ YVALLQGSHA DRSRGKRFSQ NFREVAGRFL MSETSTHLLV
sp|P57785|LFTB_MOUSE      MAIPTHVRSQ YVALLQGSHA DRSRGKRFSQ NLREVAGRFL MSETSTHLLV
sp|Q64280|TGF4_MOUSE      MVIPSHVRTQ YVALLQHSHA SRSRGKRFSQ NLREVAGRFL VSETSTHLLV

sp|O00292|TGF4_HUMAN      FGMEQRLPPN SELVQAVLRL FQEPVPKAAL HRHGRLSPRS AQARVTVEWL
sp|O75610|LFTB_HUMAN      FGMEQRLPPN SELVQAVLRL FQEPVPKAAL HRHGRLSPRS ARARVTVEWL
tr|Q8BMF7                 FGMEQRLPPN SELVQAVLRL FQEPVPRTAL RRFERLSPHS ARARVTIEWL
sp|P57785|LFTB_MOUSE      FGMEQRLPPN SELVQAVLRL FQEPVPRTAL RRFERLSPHS ARARVTIEWL
sp|Q64280|TGF4_MOUSE      FGMEQRLPPN SELVQAVLRL FQEPVPRTAL RRQKRLSPHS ARARVTIEWL

sp|O00292|TGF4_HUMAN      RVRDDGSNRT SLIDSRLVSV HESGWKAFDV TEAVNFWQQL SRPRQPLLLQ
sp|O75610|LFTB_HUMAN      RVRDDGSNRT SLIDSRLVSV HESGWKAFDV TEAVNFWQQL SRPRQPLLLQ
tr|Q8BMF7                 RVREDGSNRT ALIDSRLVSI HESGWKAFDV TEAVNFWQQL SRPRQPLLLQ
sp|P57785|LFTB_MOUSE      RVREDGSNRT ALIDSRLVSI HESGWKAFDV TEAVNFWQQL SRPRQPLLLQ
sp|Q64280|TGF4_MOUSE      RFRDDGSNRT ALIDSRLVSI HESGWKAFDV TEAVNFWQQL SRPRQPLLLQ

sp|O00292|TGF4_HUMAN      VSVQREHLGP LASGAHKLVR FASQGAP..A GLGEPQLELH TLDLRDYGAQ
sp|O75610|LFTB_HUMAN      VSVQREHLGP LASGAHKLVR FASQGAP..A GLGEPQLELH TLDLGDYGAQ
tr|Q8BMF7                 VSVQREHLGP GTWSAHKLVR FAAQGTPDGK GQGEPQLELH TLDLKDYGAQ
sp|P57785|LFTB_MOUSE      VSVQREHLGP GTWSAHKLVR FAAQGTPDGK GQGEPQLELH TLDLKDYGAQ
sp|Q64280|TGF4_MOUSE      VSVQREHLGP GTWSSHKLVR FAAQGTPDGK GQGEPQLELH TLDLKDYGAQ

sp|O00292|TGF4_HUMAN      GDCDPEAPMT EGTRCCRQEM YIDLQGMKWA KNWVLEPPGF LAYECVGTCQ
sp|O75610|LFTB_HUMAN      GDCDPEAPMT EGTRCCRQEM YIDLQGMKWA ENWVLEPPGF LAYECVGTCR
tr|Q8BMF7                 GNCDPEVPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSCL
sp|P57785|LFTB_MOUSE      GNCDPEVPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSCL
sp|Q64280|TGF4_MOUSE      GNCDPEAPVT EGTRCCRQEM YLDLQGMKWA ENWILEPPGF LTYECVGSCL

sp|O00292|TGF4_HUMAN      QPPEALAFNW PFLGPRQCIA SETASLPMIV SIKEGGRTRP QVVSLPNMRV
sp|O75610|LFTB_HUMAN      QPPEALAFKW PFLGPRQCIA SETDSLPMIV SIKEGGRTRP QVVSLPNMRV
```

```
tr|Q8BMF7                QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV
sp|P57785|LFTB_MOUSE     QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV
sp|Q64280|TGF4_MOUSE     QLPESLTSRW PFLGPRQCVA SEMTSLPMIV SVKEGGRTRP QVVSLPNMRV

sp|O00292|TGF4_HUMAN     QKCSCASDGA LVPRRLQP
sp|O75610|LFTB_HUMAN     QKCSCASDGA LVPRRLQP
tr|Q8BMF7                QTCSCASDGA LIPRGIDL
sp|P57785|LFTB_MOUSE     QTCSCASDGA LIPRGIDL
sp|Q64280|TGF4_MOUSE     QTCSCASDGA LIPRRLQP
```